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Sequence 21, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 20, Appl
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Sequence 52312, A
Sequence 77205, A
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| cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_MEMP_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEMP_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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US-09-844-864-20
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| Sequence 99, Appl Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 110, Appli Sequence 110, Appli Sequence 1110, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 11, Appli Sequence 115, Appli Sequence 11, Appli Sequence 154724, Sequence 154724, Sequence 154724, Sequence 154724,   | S   Length 1277;   Length 1277;   Length 1277;   Length 1277;   CAGTTCCACCCTGCCG 60  |
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| US-10-084-846A-99<br>US-10-084-846A-1<br>US-10-084-846A-1<br>US-10-156-761-6879<br>US-10-156-761-13<br>US-10-156-761-14<br>US-10-76-703-1498<br>US-10-76-703-1498<br>US-10-76-703-1498<br>US-10-76-703-1498<br>US-10-19-092-174<br>US-10-19-092-174<br>US-10-19-092-173<br>US-10-26-909-61<br>US-10-26-909-61<br>US-10-26-909-61<br>US-10-77-59-183<br>US-10-77-59-183<br>US-10-75-7-183<br>US-10-75-7-183<br>US-10-26-909-61<br>US-10-27-370-3<br>US-10-37-253-13<br>US-10-37-253-13<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-033-026-7<br>US-10-032-054-759-1<br>US-10-027-632-154723<br>US-10-027-632-154723   | ALIGNWENTS  14  16  1797 / OTA 99-48  1797 / OTA 99-48  1020  19/25209  19/25209  19/25209  10:  |
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GENERAL INFORMATION:
APPLICANT: Martin
APPLICANT: Martin
APPLICANT: Would with a strin
TILE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT APPLICATION NUMBER: 00/106,020
PRIOR PILING DATE: 2001-04-27
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 799.4; DB 9;
Pred. No. 1.4e-228;
0; Mismatches 1;
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Patent No. US20020042926A1
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APPLICANT: Matcuk, Martin
APPLICANT: Ren, Yongshang
APPLICANT: Ren, Yongshang
APPLICANT: Ren, Yongshang
APPLICANT: Pan, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925UGS, 0980797, OTA 99-48
CURRENT APPLICATION NUMBER: 00/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: E07/US99/25209
PRIOR PILING DATE: 1999-10-28
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                                     603 GGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCACCACCGGAGGACCGGAACAGTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGGGGGGGAGGGGGACGCACCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGGA
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Patent No. US2020042926A1

GENERAL INFORMATION:
APPLICANT: Match
APPLICANT: Match
APPLICANT: Match
APPLICANT: Match
APPLICANT: Match
APPLICANT: Match
APPLICANT: Wo, Xuemei
TILE OF INVENTY NOWARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925USZ / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: F0T/US99/25209
PRIOR PLING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FLING DATE: 1999-10-28
SOFTWARE: Patentin version 3.0

SEQ ID NO 22
LENTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.9%; Score 752.2; DB 9; Best Local Similarity 97.1%; Pred. No. 1.9e-214; Matches 778; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                           783 GGAGCGCCTGCGTTTCCAGTT 803
                                                                                                                                                                                                                                                                                                                  781 GGAGCGCCTGCGTTCCAGGT 801
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ORGANISM: mus musculus
US-09-844-864-22
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US-09-844-864-22
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LENGTH: 123
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                  SEQ ID NO 19
LENGTH: 123
                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTGTGGGGGGATGCAAGGACAAACGCCTGTCCTGCGACACCACCTTCAGCTTCAAATAC 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.90 GCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCCCCTTTCCCATTTCCAAATTCTT 249
                                           1205 CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 TTGTGTGAGAGATGCAAAAGGCCTGTCCTGCGGACAGCACCGTCAGCTTCAAATAC
                                                                       250 CATGACAGACACTTACTTAGATAAAAGCCTGTGAATAAAAGGTATTGCAAACA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGA
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                                                                                                                                                                                       Sequence 25, Application US/09844864

Patent No. US2002042926A1

GRENEAL INFORMATION:

APPLICANT: Martin

APPLICANT: Ren, Yongsheng

APPLICANT: Wh. Yongsheng

TITILE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS

TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS

TITLE NOT APPLICATION NUMBER: US/09/844,864

CURRENT APPLICATION NUMBER: 60/106,020

PRIOR APPLICATION NUMBER: 60/106,020

PRIOR APPLICATION NUMBER: PCT/US99/25209

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 25

SOFUWARE: Patentin Version 3.0

SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Matzik, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Ren, Yongsheng
APPLICANT: W. Xuemin
TITLE CANT: W. Xuemin
FILE REFERENCE: P01925US2 / 09807797 / 0TA 99-48
CURRENT APPLICATION UNMBER: US/09/844,864
CURRENT APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 260.6; DB 9;
Pred. No. 2.3e-67;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.4%;
Best Local Similarity 96.7%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: mus musculus
US-09-844-864-25
                                                                                                                                                       RESULT 5
US-09-844-864-25
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795 TTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTG 854
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                                                                                                                                                                                                                                                                                       795 TTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTG
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                                                                                                                                                                            Length 123;
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                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             69 GGAGAGGCCCTATGTGTGGTGTGTGCAGGGCACCAGTAAGGT 110
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                                                                                                                                                                                                                                                                                                                                                                                               855 GGAGAGCGCCTATGTGTGTGTGTGCAGGGCACCAGTAAGGT 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ren, Yongsheng
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 25
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APPLICANT: Wu, Xuemei
APPLICANT: Wu, Xuemei

TITLE OF INVENTION: OVAR SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
FRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
                                                                                                                                                                               Score 98.8; DB 9;
Pred. No. 4e-19;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98.8; DB 9;
Pred. No. 4e-19;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 23, Application US/09844864; Patent No. US20020049256A1; GENERAL INFORMATION: APPLICANT: Matzuk, Martin
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Patent No. US20020042926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%;
                                                                                                                                                                                    7.78;
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                               Query Match
Best Local Similarity 98.0
Matches 100; Conservative
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APPLICANT: Matzuk, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: mus musculus US-09-844-864-23
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                                                                                                  ; ORGANISM: mus
US-09-844-864-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 CCCTGCTGTCGCGGATGGGTCCCCCGGTCAGCAGCCGTGACGCTGCGGTGCAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 CCGGCGCCGCGGAATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTCTCGTCCGTGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 ACCCGCGCCGCGACG-----CCTCGGTGCAGTGTTCACTCGGGCGCCGCACGCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Score 55.2; DB 17;
Pred. No. 1.3e-05;
0; Mismatches 293;
                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_15091C.1
      FILE REFERENCE: 30-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 8597
LENGTH: 1041
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Publication No. US20040045049A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riechmann, Jose Luis
Adam, Luc J.
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Fromm, Michael E.
Heard, Jacqueline E.
                                                                                                                                                                                                                                                                                                                                                          4.3%;
Best Local Similarity 46.2%;
Matches 25%; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reuber, T. Lynne
Keddie, James S.
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Broun, Pierre E.
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                                                                                                                                                                                      TYPE: DNA ORGANISM: Oryza sativa
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Patent No. US20020042926A1

GENERAL INFORMATION

APPLICANT: Martin

APPLICANT: Ren, Yongsheng

APPLICANT: Wu, Xuemei

TILE CF INVENTION: OWARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US / 09807797 / OTA 99-48

CURRENT APPLICATION NUMBER: US/09/844,864

CURRENT FILING DATE: 2001-04-27

PRIOR FILING DATE: 1998-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.0

SEQ ID NO 24

LUSTON NUMBER OF SEQ ID NOS: 25

SEQ ID NO 24
                                                                                                                                                                                                                                              DB 9; Le
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Pred. No. 1.2e-10;
0; Mismatches 1;
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100.0%; Pred. No. 3.96
tive 0; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Thou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Local Similarity 98.6%;
nes 71; Conservative
SOFTWARE: Patentin version SEO ID NO 20 LENGTH: 105
                                                                                                                                                                                                                                                                                                      72; Conservative
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CORGANISM: mus musculus
US-09-844-864-20
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Best Local Similarity
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US-10-437-963-8597/c
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APPLICANT:
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Matches
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COURAGN PILLING DATE: 2003-02-25
PRIOR PELICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR PILLING DATE: 2001-08-22
PRIOR PPLICATION NUMBER: 09/934,455
PRIOR PPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/336,692
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-09
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 680, Application US/10374780A; Publication No. US20040019927A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
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Similarity 43.4%;
51; Conservative 0
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Ratcliffe, Oliver
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Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haake, Volker
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ORGANISM: Oryza sativa
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US-10-374-780A-680
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2011
                                                                    APPLICANT: PIGGTH, MASENA L.
APPLICANT: Creelman, Robert A.
APPLICANT: DuBell, Arnold N.
APPLICANT: Batcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION POLYMUCIC-Octides and Polypeptides in Plants
FILE REFERENCE: MB1-0048CIP (2003-04-10)
FILE REFERENCE: MB1-0048CIP (2003-04-10)
PRIOR PLILING DATE: 1990-09-13
PRIOR PLILING DATE: 1990-09-13
PRIOR PLILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/594,519
PRIOR PLILING DATE: 2000-03-22
PRIOR PLILING DATE: 2000-03-27
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Pred. No. 3.1e-05;
0; Mismatches 328; Indels
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Best Local Similarity 43.4%;
Matches 251; Conservative
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; ORGANISM: Oryza sativa
US-10-412-699B-1133
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                                                                                                    617 CCGGGTGGGAGCAGCACCACCGGAGGACCGGAACAGTGTGGGGGGGATGCAGTCTG 676
                                                                                                                                              778 CGCCGTTCGAGGAGCAGCAGGAGCAGGTGAAGGCCGAGGACAGGCTGAGCACGGCA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 CCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGG 196
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                                                  718 CGGCCGACGTGAAGGTCGCCGTCCCGGACGCCGAACCCGGCGCTGGAGGAGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Dubell III, Arnold T
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REPERBURE: MIL-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                           677 AGCCTGGGAGCGAGGCCATGTCCTGCCGCAGAGATGG 715
                                                                                                                                                                                                                                                                Score 54.2; DB 16;
Pred. No. 3.1e-05;
0; Mismatches 328;
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APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 77205
1555 GAGAGAGGCCACCCCGGGGGGGGGCCCTCGCCGTGGTGAGGAGCCGTTAGCCACC 1496
                                                                                                                                                                                                                                                                                                                                                            1375 GCGCCCGTCCCCGTCGACGCCGCCACCGCCGCGCCCCATCCCCCACCGCCGCCATCG 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 resecricesaciderrefrescescescescencircerestricades da 427
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                                                                                                                     232 CGGTCGGTCAGCAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCCGCCGACGCCTCGGTG
                                                                                                                                                                                            1495 cedecececercede adececece de concentrate de contrate de contr
                                                                                                                                                                                                                                                                                352 CGATCGGGTTCCTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT4530_77125C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(720)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 77205, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 48.2
Matches 176; Conservative
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 52312
LENGTH: 2664
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                                                                                                                                                                                                                                                                                                                      TGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAACCCCGTG 376
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                                                                       418 AGAACAAGCTGGAGCCGGAGCGGAAGACGGAGCTGGCGCGGAAGCTAGGGCTGCAGCCGC 477
478 GGCAGGTCGCCGTGTGGTTCCAGAACCGCGCGCGCGCTGGAAGACCAAGCAGCTCGAGC
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                                                                                                                                                           CGGTGCAGGTGAACCCGCGCGCGCGCCTCGGTGCAGTGTTCACTCGGGCGCCCCACGC
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4.1%; Score 52.8; DB 17; Length
Best Local Similarity 49.0%; Pred. No. 0.00011;
Matches 141; Conservative 0; Mismatches 147; Indels
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US-10-437-963-52312
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LOCATION: (1)..(2664)
OTHER INFORMATION: unsure at all n locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
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; OTHER INFORMATION: aviG4 dna: partial sequence of coding strand 1; nucleotide 1; CTHER INFORMATION: CORRESPONDED to nucleotide 45,341 of coding strand 1. US-10-084-846A-99
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GENERAL INFOGRATION:
APPLICANT: WEITHANDER, GARDES
APPLICANT: MIHENWEG, AGNES
APPLICANT: TREFEZER, AKEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
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Substitution No. US20040006026A1
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GENERAL INPORMATION:
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| copyilgic (c) 1993 - 2004 Compugen Ltd.  |   |                         | 37.1                                | 499                  |            | AI854700<br>BB703259                         |
| OM nucleic - nucleic search, using sw model  |   |                         | 32.4                                | 491                  | 0          | BB704648                                     |
| Run on: September 24, 2004, 17:12:32; Search time 3653 Seconds (without alignments) 10439.092 Million cell updates/sec |   |                         | 31.2                                | 425<br>590<br>450    |            | BB705931<br>AU023153<br>BE946858             |
| Title: US-09-830-810A-1 Perfect score: 1277 Sequence: 1 aaggcgggggggggggaacaaaaaaaaaaa                                 |   |                         | 28.8<br>28.7<br>28.7<br>20.5        | 521<br>427<br>434    |            | BB703869<br>BB706957<br>BB699732             |
|  |   |                         | 25.0<br>25.0                        | 400<br>905           |            | BB7004146<br>BB700620<br>BZ114495            |
| Searched: 27513289 segs, 14931090276 residues  |   |                         | 22.1<br>20.7                        | 301                  |            | BX637052<br>BX637052<br>BR248342             |
| Total number of hits satisfying chosen parameters: 55026578  |   |                         | 17.8                                | 642                  | 13         | BY719704                                     |
| Minimum DB seq length: 0<br>Maximum DB seq length: 200000000   |   |                         | 16.6                                | 251                  | 6000       | AV359580<br>AV358045                         |
| Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries                                  | 0 | 201.8<br>200.8<br>200.8 | 15.9                                | 2000<br>2000<br>2000 | , 2, 6, 5, | AV35/766<br>BB063113<br>AL904756<br>BX755136 |
| Database : BST:*   | 336                                     |                         | 15.6                                | 246<br>246           | 10         | BB060381<br>BB060134                         |
| 1:10   |   |                         | 15.5<br>15.5                        |                      |            | AL904892<br>BM861479                         |
| 3: em_estin:*  | 36                                      |                         | 15.4                                |                      | 12         | BJ098465                                     |
| 4: em_estmu:*<br>5: em_estov:*   | 8 6                                     |                         | 15.4                                |                      | , et       | AL904839                                     |
| 6: em_estpl:*  | 33<br>40                                | 196.8<br>196.8          | 15.4                                | 559                  | ৰ<br>তে    | AL904774<br>AL904855                         |
| 8: em_htc:*  | 41                                      |                         | 15.4                                |                      | . et       | L904863                                      |
| 9: gb_est1:*   |   | 4.96.4                  | 4.2.4                               |                      | <b>≪</b>   | AL904817                                     |
| 10: gp_est2:*<br>11: qb_htc:*  |   | . 4.                    | 15.4                                | 579                  |            | AL904816                                     |
| 12: gb_est3:*  |   | 4.                      | 15.4                                |                      |            | AL904765                                     |
| 14: gb_ests: *   |   |                         |                                     |                      |            | TI TOTAL                                     |
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|  | DEFINITION                              | BB641267<br>N BB641267  | 267<br>267 RIKEN                    | EN ful               | ]-]        | 675 bp<br>Jath enrich                        |
| 21: em gss mam:*   |   |                         | lus cDNA                            | A clon               | e A8       | clone A830014H23 5',                         |
|  | ACCESSION<br>VERSION                    | BB641267<br>BB641267.1  |                                     | GI:16476392          | 9636       |  |
| 24: em_gss_pro: *<br>25: em_gss_rod: *   | KEYWORDS                                | EST.                    |                                     | F01.15               | 600        | v  |
|  | SOURCE                                  | Mus                     | musculus (house                     | (hous                |            | mouse)                                       |
|  | כונים של אורי                           | Euk                     | mus musculus<br>Eukaryota; Metazoa; | etazoa               |            | Chordata; Crar                               |
| gb_gss2  | HERERANCE                               |                         | malia; Eutheria;                    | theria               |            |  |
| Pred. No. is the number of results predicted by chance to have a   | AUTHORS                                 |                         | wa, T., (                           | Carnino              | ci,P       | Arakawa, T., Carninci, P., Fukuda, S.        |

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secore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BB641267 BB641267 BB264222 BB264222 BG071693 H3102B03-BG084538 H3102B03-Description SUMMARIES BB641267 BB264222 BG071693 BG084538 Ð 10 10 12 Length DB 675 666 615 595 Query 50.4 50.3 46.3 Score 643 642.4 591.4 582.4 No. Result

ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 666)

2 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okada,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sagabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Sogabe,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCTCGAGACCAGGCCTCCCCCCAA 765
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URL.http://genome.gsc.riken.go.jb/
Carninci, P., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K.,
Itoh, M., Ronno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,K.,
Hayatsu,M., Aomo,H., Okazaki,Y.,
Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yomeda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 5e-87;
0; Mismatches 15; Indels 1
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/db_xref="taxon:10090"
/clone="A883014H23"
/tissue_type="Cortex"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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1068 AACGCCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCTTTAGTGAGAGTCGAAAA 1127
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This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3102 row B column: 03
Seg primer: -21M13 Forward
High quality sequence stop: 615
                                   CAGTAAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGAGAAATCCTACAACCCTTACA 947
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H3102B03-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3102B03 3', mRNA sequence.
                                                                                                                                                                                                                                          301 CAGTAAGGTG-TACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACA
                                                                                                                                                                                                                                                                                                                                               TTCGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACA
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            CACGGAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTA
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Other_ESTs: H3102B03-5
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Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 615)
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Sugahara,Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                    prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wag1,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was gAGAGAGAAGAATCCAAGAGCTTTTTTTTTTTTTTVN 3'], cDNA was
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Computational Analysis of Full-Length Mouse CDNAs Compared with
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/clone_lib="RIKEN full-length enriched, 10 days neonate
cortex"
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
Normalization and subtraction of cap-trapper-selected cDNAs to
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Pred. No. 6.2e-87;
0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A830014H23"
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/lab host="DH10B"
/clone lib="NIA Mouse 15K CDNA Clone Set"
/clone lib="NIA Mouse 15K CDNA Clone Set"
/clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone in unfertilized egg to blastocyst, embryonic part of 187.5 embryos, extraembryonic part of 187.5 embryos, and 12.5 female mesonephrosolycond and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo (dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray, 2000 Proc. Natl. Acad. Sci. U S A, 97: 9122; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
rais clone set has been freely distributed to the details.
Plate: H3102 row: B column: 03
Seq primer: -21M13 Reverse
Pich quality sequence stop: 595
POLYA-NO.
                                                                                                                                                                                                                                                                                                          595 bp mRNA linear EST 18-DEC-2003
H3102B03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3102B03 5', mRNA sequence.
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Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
76 CCTCTTCCCTTTCCAAATTCTTCATGACAGACAGTG-TACTTGGATATAAAGCCTGTGAA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jan 26, 2001 this sequence version replaced gi:12567102. Other BSTs: H3102B03-3 Contact: George J. Kargul Laboratory of Genetics
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H3102B03-5"
/db_xref="taxon:10090"
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Mus musculus
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dev_stage="Clones arrayed from a variety of cDNA
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                                                                       mol_type="mRNA"
|strain="C57BL/60"
|db_xtref="niaES":H3102B03-3"
|db_xtref="taxon:10090"
                                       organism="Mus musculus"
                                                                                                                                                                                                              clone="H3102B03"
                                                                                                                                                                                                                                                                                                                                                 lab host="DH10B"
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nes 614; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
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Normalization and subtraction: two approaches to facilitate gene
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UI-M-BH3-awu-b-08-0-UI.rl NIH BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-awu-b-08-0-UI 5', mRNA sequence.
                                                                                                                                             CCCCAGCCGCGAAGCGAGGGCGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGAGCAG
                                                                                                           181 GAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGAC
                                                                                                                                                                                                                                           CAGCCACCACCAGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCCTGGGAGCGAG
                                                                                                                                                                                                                                                                                                          GAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTGGGAGAGAGCCCTATGTG
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the X chromosome, 1998, Hum Mol Genet 7: 1967-1978.
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
6082-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                  ۲,
                                                Score 582.4; DB 12; Length 595; Pred. No. 6.4e-78;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTGTGTGCAGGCACCAGTAAGGTGTTACTTCAAACAGTTCT
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                                                                               0; Mismatches
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/db xref="Laxon:1000"
/db xref="Laxon:1000"
/db xref="Laxon:1000"
/dco="UI-M-BH3-awu-b-08-0-UI"
/dev stage="127-32 days"
/lab host="DHIOB (Life Technologies)"
/clone lib="NIH BMAP M S4"
/note="Vector: pT713D=Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco R!; The NIH BMAP M S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtracted libraries representation of cDNAs from which ESTs had already been generated in this process: NIH BMAP M S4; NIH BMAP M S3.1, NIH BMAP M S3.1, NIH BMAP M S3.2, and NIH BMAP M S3.2, NIH BMAP M S3.2, and NIH BMAP M S3.2, and NIH BMAP M S3.2, and NIH BMAP M S3.3, NIH BMAP M S3.2, and NIH BMAP M S3.3, NIH BMAP M S3.3, and Libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography into DH10R harteria (in the form of single-stranded circles contacted library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into DH10B bacteria (LifeTechnologies) to generate the NIH BMAP M S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS.
Should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGCGATGTTCAGGCTGCAGGGCA
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                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                         Location/Qualifiers
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/strain="C57BL/6J"
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Conteact: Yoshinide Hayashizaki
Conteact: Yoshinide Hayashizaki
Conteact: Yoshinide Hayashizaki
Conteact: Yoshinide Hayashizaki
Liaboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC). Yokohama Institute
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1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-92
Fax: 81-45-503-92
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Konno,H., 1757-171 (2000)

Konno,H., and Hayashizaki,Y.
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BB704019 RIKEN full-length enriched, in vitro fertilized eggs Musengues CDNA clone 7420459B08 3', mRNA sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 525)
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/note="Site 1: Salt; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5/
GAGGAGAGATCCAAGAGCTCTTTTTTTTTTTTTVN 3/], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second Strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGTTTCCAGTTCTTAGAGCAGAAATACGGCTACTATCACTGCAAGGACTGCAAAATCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGGAGAGAGCGCCTATGTGTGTGTGTGCAGGGCACCAGTAAAGGTGTTACTTCAAACAGT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer adapter of sequence [5' GAGAGAGAGATTTCCCCCCCCCC 3']. cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                    /tissue_type="in vitro fertilized eggs"
/dev stage="egg"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 497.2; DB 10 99.0%; Pred. No. 4.1e-65; ative 0; Mismatches 3.
organism="Mus musculus"
                                 /mol_type="mRNA"
/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="7420459B08"
                                                                                                                                                                    /sex="female"
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AI854700/c RESULT

Location/Qualifiers

e mouse tissues

FEATURES

81

22

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 491)
3 Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Nakamura,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura,T., et al.
                                                                                                                                                                                                                      CCACGTGGACCCTAAACGCCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB703259 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420449J15 3', mRNA sequence.
                                                                                                              CCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1192 ITTCCAAATTCTTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTA 1251
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehihro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                   200 cérérécérécéacácértréactreaaracarearraragagagacaaaacerr 141
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watshuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Mastsuuras,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                    AAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAATCCTACAACCCTTACAGAGT
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RIKEN integrated sequence analysis (RISA) system--384-format
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/mol type="mrna"

/mol type="mrna"

/mol type="mrna"

/db xref="taxn:1090"

/db xref="taxn:1090"

/clone="UI-M-EH0-akc-d-12-0-UI"

/dev_stage="27-32 days"

/lab_host="Planto (Life Technologies)"

/lab_host="Planto (Life Technologies)"

/lab_host="Planto (Life Technologies)"

/lab_host="NIH BMAP M S1"

/note="Vector: PT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: ECO R1; The NIH BMAP M S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of
     EST 15-JUL-1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized basal ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made determined the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, the record will be updated accordingly when that means is determined.
A1854700
UI-M-BHO-akc-d-12-0-UI.sl NIH BMAP M Sl Mus musculus cDNA clone
UI-M-BHO-akc-d-12-0-UI 3', mRNA sequence.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, 2089-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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TAG SEQ-TGTĀC"
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Pred. No. 1.3e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chin, H
National Institute of Mental Health
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                                                                                                                                                                                                                                                                                                                                            discovery
Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: M13 Forward POLYA=Yes.
                                                                                                   AI854700.1 GI:5498606
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Local Similarity 99.2%;
les 497; Conservative
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AUTHORS
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8 엄 ð

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1183 CCTCTTCCCTTTCCAAATTCTTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAA 1242
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/dev_stage="egg"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="7420466L07"
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Mus musculus
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                                                                                                                                                                        1243 TAAAAGGTATTGCA 1256
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Flease visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="KIKEN full-length enriched, in vitro
fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="in vitro fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420449J15"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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'lab_host="DH10B"
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BB704648 BKIKEN full-length enriched, in vitro fertilized eggs Mus musculus CDNA clone 74204666L07 3', mRNA sequence.
419 CCTCTTCCCTTTCCAAATTCTTCATGACAGAGAGG-TACTTGGATATAAAGCCTGTGAA 477
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                              Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, V., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Matsuyama, T., Okado, T., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Miramaka, T., Tomaru, A., Toyan, T., Watahiki, A., Yasunishi, A., Riken Bncyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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1243 TAAAAGGTATTGCAAAC 1259
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                                                                                      ERATO/Doi Project (Unpublished (1998)
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                            Interestite 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGACAGCACTCTTTTTTTTTTTTVN 3'; cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                     was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI"
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                     cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5, GAGAGAGAGATTCTCGAGTTAATTAATCCCCCCCCCCC 3,]. cDNA
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/clone_lib="RIKEN full-length enriched, in vitro
fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                        32.4%; Score 413.8; DB 10; Length 491; ilarity 93.0%; Pred. No. 1.4e-52; Conservative 0; Mismatches 32; Indels 2;
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0; Mismatches 32;
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AU044294.1 GI:3979844
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AU044294/C
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Systematic analyses of genes expressed in 16-cell mouse embryo (The ERATO/Doi Project at Wayne State University)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BB705931 RIKEN full-length enriched, in vitro fertilized eggs Mus
musculus cDNA clone 7420484F16 3', mRNA sequence.
                                                                                                                                                                                                      Contact: Hirofumi Doi

Contact: Hirofumi Doi

Doi Bloasymmetry Project, ERATO

Japan Science and Technology Corporation (JST)

WGG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan

Email: hd@bioa.jst.go.jp.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1123 GAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CCTCTTCCCTTTCCAAATTCTTCATGACAGACAGTG-TACTTGGATATAAAGCCTGTGAA
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                   1 (bases 1 to 436)
Ko.M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T.,
DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/clone="10917609"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Mus musculus (house mouse)
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179

119

949 09

5

1069

239

299

418

Length 590;

31.0%; Score 396.4; DB 9;

Query Match

ORIGIN

TITLE

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590 bp mRNA linear EST 20-0CT-1998 AU022153 Mouse unfertilized egg cDNA Mus musculus cDNA clone J0426F07 3', mRNA sequence.
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Ko,M.S.H. Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E. Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in unfertilized mouse eggs (The ERATO/Doi Project at Wayne State University) (Ko,M.S.H. et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al.)
Upublished (1998)
Contact: Hirofumi Doi
Contact: Hirofumi Doi
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bloa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                     180 CGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAA
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                                                                                                                         1010 CGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGACAAA
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                                                                                                                                                                                          390 GTAAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGA
                                                                                              Score 398.2; DB 10; Length 425;
Pred. No. 3.1e-50;
); Mismatches 3; Indels 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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    31.2%;
98.8%;
Query Match
Best Local Similarity 98.83
Matches 422, Conservative
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AU023153/c
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KEYWORDS
SOURCE
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Email: genome-res@gsc.riken.go.jp,
UKL:http://genome-gsc.riken.go.jp,
UKL:http://genome-gsc.riken.go.jp,
UKL:http://genome-gsc.riken.go.jp,
UKL:http://genome-gsc.riken.go.jp,
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contract: Yoshinide Hayashizaki
Contract: Yoshinide Hayashizaki
Laboratcry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
       1 (bases 1 to 425)

Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
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Muramatsu,M. and Hayashizaki,Y., Watahiki,A., Yasunishi,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="in vitro fertilized eggs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Mus musculus"
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AUTHORS
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FEATURES

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/db xref="taxon:1000"
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/note="vector: FT73D=Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco R1; The Not II: Not I; Site 2: Eco R1; The Not II: Not II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into DH10B bacteria (LifeTechnologies) to generate the NIH BMAP M S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGCGCCGCACGCTGCAGCCTGCAGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TCCTTATCCGCAGGCCACCAAGCCGGGGATGCCTGGAGGTTCGGAGCCAGGGGCTGCCG
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Pred. No. 1.9e-49;
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                                                                                                                                                         /mol_type="mRNA"
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            Seq primer: M13 Forward POLYA=No.
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99.7%;
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Matches 393; Conservative
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                                                                                                     source
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
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                                                                                   TGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGGCAAAGCACGG 772
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-M-BH3-awu-b-08-0-UI.sl NIH BWAP M S4 Mus musculus cDNA clone UI-M-BH3-awu-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TTTCTGNTAGATGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTTTC
                                                                                                                                             542 IGGNCTNAGACCCCCCTTATTCGGATGCCCCTGGAACAGGCNTCCCNCAANNCCGGACC
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                                    Gaps
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
                                                                                                                                                                                                        773 AGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGG-
                                 Indels
   5.3e-50;
ches 71;
                              0; Mismatches
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   Pred. No.
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BE946858.1 GI:10524617
86.18;
                              464; Conservative
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Fax: 301 443 9890
Best Local Similarity
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AUTHORS
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ACCESSION

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GEO), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

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URL:http://genome-res@geo.riken.go.jp,
URL:http://genome-res@geo.riken.go.jp,
Carminci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
Carminci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

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Matahiki,M., Yoneda,Y., 16hikawa,T., Togawa,K., Tanaka,T.,
Matahiki,M., Yoneda,Y., 16hikawa,T., Togawa,K., Tanaka,T.,
BIKEN, Hayashizaki,Y.,
BIKEN, Hayashizaki,Y.
                                                                    BB704449 BIXEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420464A04 3', mRNA sequence.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 419)
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Hasuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.
Tanaka, T., Tomaru, A., Tayawa, A., Takahashi, F., Takaku-Akahira, S.,
Muramatsu, M. and Hayashizaki, Y. Watahiki, A., Yasunishi, A.,
REKEN Broyclopedia of Mouse Full-length cDNAS (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="egg"
/lab_host="DH10B"
/clone lib="RIKEN full-length enriched, in vitro
fertilized eggs" cite 2. RamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="in vitro fertilized eggs"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                 DEFINITION
RESULT 14
BB704449
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FEATURES

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 521)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Matsuyama,T., Nakamura,M., Nojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sagaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                            BB703869 RIKEN full-length enriched, in vitro fertilized eggs Musmusculus CDNA clone 7420457C21 3', mRNA sequence.
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                953
contributed to prepare mouse tissues. 1st strand cDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 TCCAAATTCTTCATGACAGACAGTG-TACTTGGATATAAAGCCTGTGAATAAAAGGTATT
                                                                                                                                                                                                                                                                                                                                                           894 GGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGG
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7
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Pred. No. 2.5e-49;
0; Mismatches 3; Indels 2:
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                                                                                                                                                                                                                         30.7%;
98.8%;
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Best Local Similarity 98.8
Matches 416; Conservative
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Tel: 81-45-503-9222
Fax: 81-45-503-9222
Fax: 81-45-503-9222
Fax: 81-45-503-9226
Email: genome-reseggec.riken.go.jp,
URL:http://genome.gec.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,W., Chara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.
matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-171 (2000)
KOMDO,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugabara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                      Contact: Yoshihide Hayashizaki
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AY191415 Mus muscu AY283175 Rattus no AY193889 Mus muscu AC122733 Mus muscu AJ335296 Homo sapi AF429315 Homo sapi ACL23764 Homo sapi AF429315 Homo sapi AL684264 Penicilli ACM48354 Homo sapi ACL15880 Mus muscu AL939120 Streptomy AC092857 Rattus no AC142070 Rattus no AC137771 Homo sapi AC118627 Mus muscu BX470223 Zebrafish BX69785 Danio rer BX594044 Danio rer AL684455 Penicilli AL355176 Mouse DNA AJ335067 Homo sapi BX640474 Danio rer AL671880 Mouse DNA Rattus no Rattus no Mus muscu Homo sapi Streptomy Rattus no Homo sapi Homo sapi Homo sapi Homo sapi Danio rer Zebrafish Rattus no Mus muscu Xenopus l Danio rer AC108380 Pan trogl AX655393 Sequence rakifugu score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AC127083 F AC108848 N AC108848 N AC10848 N AY283176 X AY283177 T AY283178 N AC070797 N AC070797 N AC03743 F AC193890 N AC141024 I SUMMARIES AL671880 AC107686 AC126519 AC125993 AC127083 AC108848 AC108848 AC108848 AF429315 PM11H12G AC048354 AC115880 SCO939120 AC141024 AC108380 AX655393 AC092857 AY283175 AY193889 BX537133 HSA335296 AY191415 AC092163 AY193890 AC096952 BX571888 AF429315 AC123764 AC137771 AC118627 BX470223 BX569785 BX548044 AY283177 AY283178 AC037443 10 B

ALIGNMENTS

HSA335067

PM12D6G

AL684370 Penicilli

Mus musculus zygote arrest 1 (Zarl) mRNA, complete cds.
AY191415.1 GI:27808689 Wu,X., Viveiros,M.M., Eppig,J.J., Bai,Y., Fitzpatrick,S.L. and Matzuk,M.M.
Zygote arrest 1 (Zarl) is a novel maternal-effect gene critical for Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1260) Mus musculus (house mouse) Mus musculus TITLE

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Rattus norvegicus (Rattus norvegicus)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
CCGTTCTCGTCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGAGGCAG
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Mu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M.
Sygote arrest 1 (zar1) is an evolutionarily conserved gene expressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
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LMAAEYUDSHQRAQLMALLSRWGPRSVSSRDAAVQVRPRRDASVQCGETGRRFULGPAGC
RAASPDARSGSCQPRGARGAGRS PRSWGTVAPPSSVTPCGLSSSLEVAGGRQTPTKGBG
SPASSGTREPEPREVAARKAVPQPRSEEGDVQAAGQAGWEQQPPPEDRNSVAAMQSEP
SSEBEVCPASRANAQDPRDSDARDQASSPQSTRQDYGRELRFQFLEQKYGYYHCKDCKIRW
BSAVWCVQGTSKVYFKQFCRYVCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
PHRQDLCGRCKDKRLSCDSTFSFKYII"
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                                                                                                                                                                                                                                                                                                                                                                                     /note="ZAR1; maternal factor; contains atypical C8 PHD motif at C-terminus"
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                                                                                                                      Baylor College of Medicine,
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Pred. No. 2.8e-248;
0; Mismatches 1;
                                                                                                                                                                                                                                                                       /map="between D5Buc48 and Txk"
                                                                  2 (bases 1 to 1260)
Wu,X., Wang,P. and Matzuk,M.M.
Direct Submission
Submitted (04-DEC-2002) Pathology, B.
Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="zygote arrest 1"
/protein_id="AAO24706.1"
/db_xref="G1:27808690"
   the oocyte-to-embryo transition
Mat. Genet. 33 (2), 187-191 (2003)
22447938
12539046
                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="129/SvEv"
                                                                                                                                                                                                                                        db_xref="taxon:10090"
chromosome="5"
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/gene="Zar1"
1. .27
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gene="Zar1"
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28. .1113
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Best Local Similarity 99.8%;
Matches 1257; Conservative
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(Zarl) gene, complete cds.
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Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3987)
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                                                                                                         603 CCAGGCTGAAGGGCAGGATG---GGCAGGAGCAGCCACCGCGGGAGAACCCGGACAGTGT
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                                                    600 TCAGGCTGCAGGCAGGCCGGGTGGGAGCAGCAGCACCACCACCGGAGGACCGGAACAGTGT
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Matzuk,M.M.
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Wu,X. and Matzuk,M.M.
Direct Submission
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AUMAAFYPDSYQRAQLWALLSRWGFRFPSRRDAAVQWRFRASAVQCSLGRFTLQPGR
RRASPDARPGSCQPRSPARAGRPPRSWRTVALYSPYTPGGLSSLEWAGDPTKGG
GRPAPTGTREPEPGEVAWWKAVPQPQSEEGDVQAEGODGQEQPPREDPDSVAAMGSEG
SSEEPPPAYSRAQDPSWAASRDRASPQSTEGDVERLRFQFLEGCYGYYHCKDCNIRW
ESAYWWCVQGTSKYVFKQPCRYCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
PHRQDLCGRCKDKRLSCDSTFSFKYII"
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                                            2 (bases 1 to 1280)
Wu,X. and Matzuk,M.M.
Direct Submission
Submitted (24-APR-2003) Pathology, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
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Pred. No. 1.9e-189;
0; Mismatches 143; Indels 12;
                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="zygote arrest 1"
/protein_id="AAP37037.1"
/db_xref="G1:30908933"
                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="Zarl"
'note="maternal factor"
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Best Local Similarity 87.7%;
Matches 1110; Conservative
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g ð d à g à qq ð Ωp à QD  $\delta$ g  $\delta$ qq à g

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Birren, B., Lusten, M., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J. Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P. DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, N., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyete, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Landers, T., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Macdonald, P., Major, J., Marquis, N., Macdan, C., Macdonald, P., Major, J., Naylor, J., Nguyen, C., Mitol, R., Micol, R., Ray, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, J., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Trayis, N., Trigillo, J., Tepham, K., Travers, M., Travis, N., Trigillo, J.,
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Mus musculus clone RP24-506B15, WORKING DRAFT SEQUENCE, 21
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-506B15
CGGGCGCCGCACCTGCAGGCTGCAGGGTGCCGACCCCAACCCCGACGCCCGATCGGGTTC
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ESAYVWCVQGTSKVYFKQFCRVCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
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Wu,X. and Matzuk,M.M.
Wu,X. and Matzuk,M.M.
Submitted (21-3AN-2003) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Sequence update by submitter
On Jan 21, 2003 this sequence version replaced gi:27808693.
Location/Qualifiers
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note="oocyte-specific"
codon_start=1
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/db_xref="GI:27808694"
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108523: contig of 14249 bp in length
108623: gap of 100 bp
122796: contig of 15173 bp in length
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147661: gap of 100 bp
147464: contig of 23065 bp in length
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                                               Direct Submission

All Submitted (32-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 147464)

RS Sirren, B. Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H. M., Cooke, P., Corum, B., Dekrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, K., Maclagan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Macdonald, P., Major, J., Manning, J., Matthews, C., Mccarthy, M., Madorim, J., Manning, J., Matthews, C., Mccarthy, M., Madorim, J., Manning, J., Matthews, C., Mccarthy, M., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Pererson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Sevary, P., Smith, C., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Zenbe, M., Milson, B., Wu, X., Wasiliev, H., Venkataraman, V. S., Vael, R., Vo, A., Wilson, B., Wu, X., Direct Submission

All Submitted (02-FEB-2003) Whitehead Institute/MIT Center for Genome On Feb Z. 2003 this sequence Version replaced gi:21206317.

All repeats were identified using Redesignsery
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 144000; agarose-fp
Insert size: 145464; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 140214 bases at least Q0 Consensus quality: 144454 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 653 bp in length contig of 100 bp in length contig of 1181 bp in length gap of 100 bp contig of 29962 bp in length contig of 890 bp in length contig of 890 bp in length gap of 100 bp contig of 725 bp in length gap of 100 bp contig of 1188 bp in length gap of 100 bp gap of 100 bp
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Web site: http://www-seq.wi.mit.edu
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AUTHORS
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COMMENT

misc\_feature

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems. BMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shotgun may have been used to confirm this sequence. Sequence data from the whole genome shedgun alone has only been used where it has a phred quality of at least 30.
Mouse DNA sequence from clone RP23-384C22 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was mede to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Sequence from the Mouse Genome Sequencing Consortium whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-384C22 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VBCTOR: pBACe3.6
                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                               Direct Submission
Submitted (27-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 28, 2002 this sequence version replaced gi:22204349.
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Pred. No. 1.1e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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                                                                                                            Mus musculus (house mouse)
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Van Hellmond, Z.
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Best Local Similarity 99.9%;
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        /note="assembly_fragment"
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/note="assembly_fragment"
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ROD 27-NOV-2002

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Gaps

| Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McKernan, K., Maddrim, J., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., Meddrim, J., Meneus, L., Mihova, T., McKernan, K., Meddrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.G., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Ye, Wu, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA and sess 1 to 168073)  Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastlen, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grada-Pierre, N., Hagopian, D., Hagos, E., Hall, J., Horton, L., Hulme, W., Hillev, I., Johnson, R., Johnson, K., Liu, G., Lui, X., Mabhitt, R., Machean, C., Macdonald, P., Malor, L., Mihora, T., Malor, J., Marchews, C., Macdonald, P., Malor, L., Mihonga, T., Malor, T., M | <b>₹</b>   | Center project Information  Center project name: 11749  Center project name: 12749  Center project name: 28 B 12  Center clone name: 28 B 12  Center clone name: 28 B 12  Center clone name: 28 B 12  Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrapy version 0.560731  Consensus quality: 16674 bases at least Q40  Consensus quality: 167176 bases at least Q20  Consensus quality: 167318 bases at least Q20  Insert size: 140000; agarose-fp  Insert size: 140000; agarose-fp  Insert size: 16743; sum-of-contigs  Quality coverage: 12.4 in Q20 bases; sum-of-contigs  **NOTE: This is a 'working draft' sequence. It currently  **consists of 7 contigs. Gaps between the contigs  ** are represented as runs of N. The order of the pieces  ** is believed to be correct as given, however the sizes  ** of the gaps between them are based on estimates that have  ** provided by the submittor.  ** This sequence will be replaced  ** by the finished sequence as soon as it is available and  ** the accession number will be preserved.  |
|--|--|--|
| TITLE<br>JOURNAL<br>REFERENCE<br>AUTHORS   | TITLE<br>JOURNAL<br>COMMENT  |  |
| 131304 ACCCGCGCCCCCCCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA 131363   QY  | 603 GGCTGCAGGCCGGGTGGGAGCAGCACCACCGG  131784 GGCTGCAGGCCAGGCCGGGTGGGAGCACCACCGG  663 GGCGATGCAGGCCGGGTGGGAGCAGCAGCCACCGG  131844 GGCGATGCAGTCTGAGCCTGGGAGCAAGCCATGTCCTG  723 CCCCGGTGATTCGAATCCTCAGACCAGAGCAAGCCATGTCCTG  724 CCCCGGTGATTCGAATCCCCTCGAGACCAGGCCTCCCGG  725 CCCCGGTGATTCGAATGCCCCTCGAGACCAGGCCTCCCCGG  787 GGAGCGCCTGCGTTTCCAGTT 803  131964 GGAGCGCTGCGTTTCCAGTT 19984 | DEFINITION MUS musculus chromosome 5 clone RP24-228B12 map 5, WORKING DRAFT SEQUENCE, 7 ordered pieces.  ACCESSION ACLO7686.3 GI:38424195 ACLO7686.3 GI:38424195 ACLO7686.3 GI:38424195 ACCESSION ACCESSION ACLORED MOUSE MOUSE MUSCULUS (ACCESSION) ACCESSION ACCESS |

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Allen, C., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayagi, A., Baca, E., Baden, H., Balderchi, W., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Balderdon, S., Brach, F., Balderon, B., Graderon, S., Chavez, D., Chavez, D., Chen, G., Chen, R., Casar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Toyle, M., Chen, R., Farser, C., Egan, R., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Ganta, R., Garte, R., Garter, M., Gabisi, A., Ganta, R., Garter, M., Garter, M., Gabisi, A., Ganta, R., Gardy, M., Guerra, W., Gabisi, A., Ganta, R., Henderson, W., Henrandez, W., Howells, S., Hladun, S.L., Henderson, N., Hernandez, M., Howells, S., Hladun, S.L., Hodgson, A., Hoguera, M., Jackson, J., Jackson, L., Jacob, L., Jacob, M., Liu, Y., London, P., Lowis, L., Li, Z., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Lud, L., Loodon, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louloseged, H., Martin, R., Ma
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Rattus norvegicus clone CH230-159N5, WORKING DRAFT SEQUENCE.
AC126519
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                             53926 GCAGACACCCAGGAAGGGAGAGGGAGCCCGGCATCCTCGGAGACCCGGGAACCGGAGCC
                         CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                     3491: gap of 100 bp
11221: contig of 7730 bp in length
11321: gat of 100 bp
20171: contig of 8850 bp in length
20271: gap of 100 bp
48821: contig of 25550 bp in length
45921: gap of 100 bp
100777: contig of 54856 bp in length
100877: gap of 100 bp
144569: gap of 100 bp
14569: gap of 100 bp
166073: contig of 24592 bp in length
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bp in length
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/clone_lib="RPCI-24 Male Mouse BAC"
|1. .3391
/note="assembly_fragment
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Pred. No. 6.7e-133;
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:10090"
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 20, 2002 this sequence version replaced gi:23195602.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.ngsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindarter,A., Perez,L., Pfannkoch,C.,
River,C., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Sneed,A., Sodergren,B., Song,X.-Z., Soctt,G., Shatsman,S., Shen,H.,
Sneed,A., Sodergren,R., Sutton,A., Tabor,P., Usmani,K.,
Valas,R., Veray,V., Villasana,D., Waldker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,U.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., Von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working daraft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.990129
Consensus quality: 216235 bases at least Q40
Consensus quality: 218057 bases at least Q30
Consensus quality: 218057 bases at least Q30
Estimated insert size: 221344; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
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Center clone name: CH230-159N5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 235390)
Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26989 CAGGCAGACGCCCACGAAGGGAGAGAGAGACCGGCACCCACGGGGACCCGGGAACCCGA 26930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27349 CAGGCCCGAGCCCCCCTCCTCCTCCCCGGCTACAGCACAGCTCATGGCCGCGGAGTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 ACTCGGGCGCCGCACGCTGCAGCCTGCAGGTGCCGAGCCGAGCCCCGAACGCCCGATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27109 TTCCTGCCAACCCCGCAGCCCCGCCAGGCCCGGGAGACCCCCGCGCGATCCTGGCGCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTTATCCGC---AGGCCACCACCAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CAGCAGCCGTGACGCTGCGGTGAACCCGCGCCGCGACGCCTCGGTGCAGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 AGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 TCAGGCTGCAGGCCAGGCCGGGTGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCCGGCCGAGCCCCGGCACCCATGTTCCCGGCGAGCACGTTCCACCCTGCCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 CAGGCAGACACCCACGAGGGGAGAGGGGAGCCCGGCATCCTCGGGGGACCCGGGAACCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 GCCGAGAGAGGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAAGGAGGCGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 TICCTGICAACCCCGIGGCCACGCCGGCGCCGGGAAICCCCGCGAICCTGGCAGACCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235390;
235390: contig of 235390 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 628; DB 2; I
Pred. No. 4.6e-120;
                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                    end sequence:BH321013"
complement (227221. .228048)
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                         1. .1856
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                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_end_extension
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clone_end:T7
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.1%;
Matches 708; Conservative
                                                                                                                             misc_feature
                                                                                                                                                                                misc_feature
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Direct Submission

Submitted (10-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23056451.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the facture table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                        Submitted (02-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 237695)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)
* NOTE: This is a "working draft' sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* the accession number will be preserved.
* the accession number will be preserved.
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Assembly program: Atlas 3.0;
Consensus quality: 229641 bases at least Q40
Consensus quality: 231444 bases at least Q20
Consensus quality: 235679 bases at least Q20
Estimated insert size: 242796; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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complement(234275. .235086)
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clone_end:T7"
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/note="clone_boundary
clone_end:T7
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                                                                                                           Direct Submission
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                                                                                                                                       Unpublished
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1 (Dases I Co. 23/895).

2 (Dases I Co. 23/895).

2 (Dases I Co. 23/895).

3 (Allen, C., Allen, M., Alabrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, M., Alabrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Anguiano, D., Barataedehi, V., Bair, V., Bair, V., Bair, V., Bair, V., Barateed, M., Benahmed, F., Bladwin, D., Barateed, M., Benahmed, F., Barati, N., Bair, V., Bair, V., Barateed, M., Cree, A., D'Souza, L., Carach, C., Corkel, M., Cree, M., D'Souza, L., Carach, D., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chen, Z., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chacko, J., Chavez, D., Deramo, C., Davin, M., Cree, M., D'Souza, L., Davila, M., Davis, C., Davis, M., Cree, M., D'Souza, L., Davis, M., Davis, C., Davis, M., Davis, C., Parandez, J., Falley, M., Elago, M., Porbes, L., Foater, M., Garca, M., Gabra, M., Carach, M., Garta, M., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, B., Howells, S., Huly, S., Hune, J., Idlabird, D., Jackson, A., Jackon, L., Jang, H., Johnson, R., Mandrin, M., Malloy, S., Kelly, M., Malloy, M., Strong, M., Ren't, M., Perez'n, Mangun, M., Malloy, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong,
                                          AC125993 237695 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-74L11, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
   660 GGCGGCGATGCAGTCTGAGCCTGGGAGGAGCCATGTCCTGCCGCAGAGATGGCTCA
                                                                                                                                           720 GGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC125993.3 GI:30522839
HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                   26692 CAAGGAGGCCTGCGTTTCCAGGT 26669
                                                                                                                                                                                                                                                                                   780 CAAGGAGCGCCTGCGTTTCCAGTT 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
AC125993/c
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DEFINITION
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VERSION
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ORGANISM
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AUTHORS
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                          CCGACCCGCCCCCCCTCCTCCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                122773 CAGCAGCCGCACACTGCGGTGCAGCTGAACCCGCGCCCCGCGATGCCTCGTGCAGTGTTC
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                                                                                                                                           GGCGGGCGAGGCGCGCGACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA
                                                                                                                                                                                                 TCCTTATCCGC----AGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTG
                                                                                                                                                                                                                                                                                                                   CGACAGCCACCAGGGGGCACAGCTCATGGCCCTGCTGTCGCGGATGGGTCCCCGGGTCGGT
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                                                                                                                   Gaps
                                                                                                                  9
                                                                                    Length 237695;
                                                                                  Score 628; DB 2; Length 23
Pred. No. 4.6e-120;
0; Mismatches 90; Indels
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                                          end_sequence:BH339393"
/note="clone_boundary
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             clone_end:Sp6
site:EcoRI
                                                                                  Query Match
Best Local Similarity 88.1%;
Matches 708; Conservative
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AC127083

262139 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-69F8, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 moordered pieces.

AC127083

AC127083/c LOCUS DEFINITION ACCESSION

RESULT 9

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NETTINGS NOT THOSE PRASES INTO A CHARGE STATES.

SOURCES

Rettis norvegicus (Norway zat)

Rett
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Mus musculus clone RP23-300K5, WORKING DRAFT SEQUENCE, 36 ordered
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Birran, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dadge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                      236971 TTCCTGCCAACCCGCAGCCCGCCAGGCCGGGAACCCCCGCGATCCTGGCGCACCGT
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                                                                                                                                                                                                                                                     CAGCAGCCGTGACGCTGCGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                 300 ACTOGGGGGGGGCACCTGCAGCCTGCAGGTGCCGAGCCCCGACGCCCCGATCGGG
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-300K5
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AC108848.2 GI:20336129
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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ORGANISM
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AC108848
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TITLE
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AUTHORS
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conterr project Information
Center project name: CH230-69F8
Center clone name: CH230-69F8
Center clone name: CH230-69F8
Consensus quality: 200303 bases at least Q40
Consensus quality: 200310 bases at least Q30
Consensus quality: 209370 bases at least Q20
Consensus quality: 209370 bases at least Q20
Consensus quality: 209370 bases at least Q20
Consensus quality: 209370 bases; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
       and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads both and indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Landers, T. Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J.,
Retra, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, M.,
Troplam, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H.,
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Shipmirra, A., The Shipmirra, A., The Shipmirra, Young, G.,
Shipmirra, Y., The Shipmirra, Young, G.,
Shipmirra, Y., The Shipmirra, Young, G.,
                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (131-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 212848)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Bakten, B., Linton, L., Romeria, J., Campopiano, A., Chang, J., Chargelo, M., Calmopiano, A., Chang, J., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P., FitzHudh, W., Gangel, D., Galagan, J., Gardyna, S., Ginde, S., Govete, P., Lander, M., Graph, C., Gardyna, S., Ginde, S., Govete, P., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Karatas, A., Karatas, A., Karatas, A., Maratas, A., Marchews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, W., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, P., Pierre, N., Pollara, V., Phukhang, P., Pierre, N., Pollara, V., Phukhang, P., Pierre, N., Pollara, V., Seaman, S., Severy, P., Spencer, B., Stanger, These C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Filey, R., Stanger, S., Theodore, J., Viel, R., Vo, A., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Yenny, G., Vonny, C., Volla, M., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Lainoun, J., Zembek, L., Zimmer, A. and Zody, M., Vonny, C., Subnission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 01 Apr 28, 2002 this sequence version replaced gi:18450109. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 36 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert sizė: 209348; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 206302 bases at least Q30 Consensus quality: 208218 bases at least Q30 Consensus quality: 208218 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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JOURNAL
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100 bp of 815 bp in length

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3591 bp in length 5908 bp in length

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100 bp

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Location/Qualifiers

FEATURES

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for

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                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I. (bases 1 to 1275)
Wu.X., Viveiros, M.M., Eppig, J.J., Bai, Y., Fitzpatrick, S.L. and Matzuk, M.M.
                                                                                                                                                    Zygote arrest 1 (Zarl) is a novel maternal-effect gene critical
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                                                                                                                                                                                                                                   2 (bases 1 to 1275)
Wu,X., Bai,Y. and Matzuk,M.M.
Direct Submission
Submitted (04-DEC-2002) Pathology, Ba
Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                              the occyte-to-embryo transition
Nat. Genet. 33 (2), 187-191 (2003)
22447938
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Homo sapiens
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Homo sapiens zygote arrest 1 (ZAR1) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 360; DB 2; Length 212848;
Pred. No. 2.1e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94230 GTGTCCTGCTGCTGCAGAGATGGCTCAGGACCCCGGTGACTCGGATGC
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1. .641
                                                                                                                                                                                                                                                                                                                 076. .10257
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Best Local Similarity 91.7
Matches 429; Conservative
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Mus musculus clone RP23-300K5, WORKING DRAFT SEQUENCE, 36 ordered
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 212848)
                                                                                                                                                                 891 GGAGGGGCCGTCGCGGGAGAGGGCCGTCGCCACGGAGCCCGGAGCTGGGCAAAGAAG
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-300K5
'O'ULLIShed
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KEYWORDS
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Direct Submission

Submitted (31-JNA-2020) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 212848)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N. Bastien, V., Bloom, T., Boguslavkiy, L., Chararate, B., Erown, A., Camarate, J., Campopiano, A., Chang, J., Characio, K., Dawar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gorde, S., Gorde, M., Craham, L., Grand, Pleire, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mayuguis, N., Mathews, C., McCarthy, M., McEwan, P., Major, J., Mayuen, C., Nicol, R., Mison, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schueback, R., Stander, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainonn, J., Zembek, L., Zimmer, A. and Zody, M., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Leite, S., Wu, X., Wyman, D., Ye, W.J., Young, G., Leite, S., Leite
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIS
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Center clone name: 300 K 5

------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
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* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1742 1421: contig of 641 bp in length

* 1428 1527: gap of 100 bp

* 1528 3170: contig of 1643 bp in length

* 1528 3170: contig of 1643 bp in length

* 3271: gap of 100 bp

* 3271: gap of 100 bp

* 3496: contig of 1126 bp in length

* 3497 4496: gap of 100 bp
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88151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTTATCCGCAGGCCACCAAAGCCGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCCCCCCCCCCCTCCTTCCTCCCCCGCTACAGACAGCTCCATGGCCGCGCGGAGTACGTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 212848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
70 183469: gap of 100 bp
70 210291: contig of 26822 bp in length
72 210391: gap of 100 bp
72 212848: contig of 2457 bp in length.
10 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                    /clone="RP23-300K5"
/clone lib="RPCI-23 Female Mouse BAC"
1. ,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 299.8; DB 2;
Pred. No. 6.8e-52;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
13390. 15335
                                                                                                                                                                                                                                                                            6010. .7583
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                      15436. .16250 //note="assembly_fragment"
|16351. .17669
                                                                                                                                                                                                            /note="assembly_fragment"
3271. .4396
                                                                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                     1497. .5909
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                              note="assembly_fragment"
                                                                                                                                                                          742. .1427
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                  1. 212848
/organism="Mus musculus'
/mol type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 310; Conserv
     183370
183470
210292
210392
                                                                                                                                               misc_feature
                                                                                                                                                                                                     misc_feature
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                                                           FEATURES
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linear VRT 21-AUG-2003 mRNA, complete cds.
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VRELRRRKLNPGPPGTPQKTEGSVRYPRTLAVSBIAFRSYTSFLVBTGKDRPAAE
AQAELPGEQPEQKGGENQAGEETNANLPEGRKPQSEDAQTAADAEGSKGKARVRPQF
LEQKYGYYHCRECNLEWBSAYWCVQGTNKVYFKQFCRKCQKDFNPYRVEDITCHVCN
KARCACAETQRHVDPKRPHRQDLCGRCKGKRLSCDSTFSFKYIV"
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                                                                                                                                                                                                      Takifugu rubripes (rugu rubripes)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
1 (Bases I to 963)
Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M.
Zygote arrest 1 (zarl) is an evolutionarily conserved gene expressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                      To the seas 1 to 963)

Wu.X. and Matzuk, M.M.

Direct Submission

Submitted (24-APR-2003) Pathology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MATYCDEPVDSYFYSSYNPYMGRYPRHRDAGWKYKSYLSHYGDT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 AGGCAAAGCGCGTGTCCGCTTCCAGTTTCTGGAACAGAAGTACGGCTACTATCACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 Gagaaridcaaccrigcgarigggagaggcgcgracgrrrrggrgcgrrcagggcacraaaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 TGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAAACCCTTACAGAGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGAGATGCAAGGACAAACGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 194.8; DB 5; Length 963;
Pred. No. 4.7e-30;
0; Mismatches 82; Indels 1
                                                                                        Takifugu rubripes zygote arrest 1 (Zarl)
AY283177

    .963
    /organism="Takifugu rubripes"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="zygote arrest 1"
/protein_id="AAP37039.1"
/db_xref="GI:30908937"
                                                                                                                                                                                          Takifugu rubripes (Fugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Zar1"
/note="maternal factor"
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                                                                                                                                                    AY283177.1 GI:30908936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Zarl"
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Best Local Similarity 75.4'
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .963
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                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
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PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                          RESULT 14
                                                                        AY283177
LOCUS
                                                                                                                                                                                                                                                                                                          REFERENCE
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QLKAILSQVNNNLTPRLCRANTRDVGVQVNPRQDASVQCSLGPRTLLRRRPGALRKPP
PEGGSPASPYRTVYRPRTTAVYSPYPAGRLAPPODGVNLEEKGBARSEGSEGGRQF
GKQGTGCEIKEQMKMNYTDEERAAPAQTRPKFQFLEQKYGYYHCKDCNIRWESAYVWCV
QETNKVYFKQFCRTCQKSYNPYRVEDIMCQSCKQTRCACPVKLRHVDFKRPHRQDLCG
RCKGKRLSCDSTFSFKYII"
                                                      21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .036 TCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCACCTTCAG 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         713 CAGGACAIGICAGAAAICCIATAAICCIACCGIGIGGAAGACAICAIGAGIGAGAGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 CAAGCAGACGAGATGCGCGTGTCCTGTCAAACTGCGTCACGTTGACCCCAAGAGGCCCCA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICCAGTICITAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGCGCCTATGTGTGGTGTGTGCAGGCACCAGTAAGGTGTTACTTCAAACAGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               654 GAGAGCGCCTACGTGGGGGTGTGCGGGAAACCAATAAGGTG-TACTTCAAGCAGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  976 TAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594 Trccagriccigaagcagaagracggararrarcacrgraaggacrgcaacarccecrgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                        gene
                                                                    (Zarl) mRNA, complete cds.
                                                                                                                                                                                                                                                                  Matzuk, M.M.
                                                      VRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1052;
                                                                                                                                                                                                                                          1 (bases 1 to 1052)
Wu,X., Wang,P., Brown.C.A., Zilinski,C.A. and Matzuk,M
Zygote arrest 1 (zarl) is an evolutionarily conserved
expressed in vertebrate ovaries
                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 205.8; DB 5;
Pred. No. 2.4e-32;
0; Mismatches 62;
                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1052)
Wu,X. and Matzuk,M.M.
Direct Submission
Submitted (24-APR-2003) Pathology, Be
Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Biol. Reprod. 69 (3), 861-867 (2003)
22811438
                                                                                                                                          Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="zygote arrest 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAP37038.1"
/db_xref="G1:30908935"
                                              1052 bp
Xenopus laevis zygote arrest 1 (
AV283176
AV283176.1 GI:30908934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="maternal factor"
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                                                                                                                                                                                                                            Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Zarl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="Zarl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.1%;
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052
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YFDNHHRAQLKSILSQINPNLTPRLEKANTKDVGVQNNPKTDASIQCSLGPRTLLARK
TETALERREGETVGTPGSPVSSGGVRFPTQAVYSPVESRLVSLFREGGEEEDTDLEV
TETYDASEKLESAERUSSGOVRFPKKARAKQLSFEKNINKQTETNEENTNEPVKTSQDDLK
SKARVRFQSLEQKYGFYHCKDCNLRWESAYVWCVQGTNKVYFKQFCRTCQKSFNPYN
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                                                                                                                                      AY283178 1084 bp mRNA linear VRT 21-AUG-2003 Danio rerio zygote arrest 1 (zar1) mRNA, complete cds. AY283178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-APR-2003) Pathology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
1. 1084
/organism="Danio rerio"
/mol type="mRMA"
/db_xref="taxon:7955"
1. 1084
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                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

(bases 1 to 1084)

Wu,X., Wang, P., Brown, C.A., Zilinski, C.A. and Matzuk, M.M.
Zygote arrest 1 (zarl) is an evolutionarily conserved gene expressed in vertebrate ovaries
Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDIACQTCKKARCTCSVKSRHVDPKRPHRQDLCGRCKGKRLSCDSTFSFKYII"
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1076 TCCTCCGACACCACCTTCAGCTTCAAATACATCATTA 1113
925 TCCTGCGACAGCACCTTCAGCTTCAAATACATCGTCTA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="zygote arrest 1"
protein_id="AAP37040.1"
db_xref="GI:30908939"
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'note="maternal factor"
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42. .1031
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Wu, X. and Matzuk, M.M.
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Db 931 ACGTGGACCCATCGGCAGGATCTCTGCGCGCTGTAAAGGCAAGCGTC 990
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Db 991 TGTCCTGCGACACGTTCAGCTTCAAATACATCATTAG 1131
Search completed: September 24, 2004, 19:00:12
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Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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N\_Geneseq\_29Jan04:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* Database

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description |        | Aad00294 Mouse ooc |          | Abz24590 Mouse ova | Abz24591 Mouse ova | Abz24592 Human ova | Aax53491 Human ade | Ada71938 Rice gene | Ada69587 Rice gene |          | Abz37562 Streptomy |          | Abz37515 Streptomy | Aav44436 Mycobacte | Aav64545 M. tuberc | Aaz19134 M. tuberc | Aaz19346 M. tuberc | Abl66291 Lung canc | Aas94858 Human DNA | Aag84658 Human neu | Aav42686 DNA encod | Aaa71704 Human cal | Aad39956 Human cal | Abz58367 Human N-t |
|-----------|-------------|--------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES |             | ID     | AAD00294           | ABZ24589 | ABZ24590           | ABZ24591           | ABZ24592           | AAX53491           | ADA71938           | ADA69587           | AAX53491 | ABZ37562           | ABZ37516 | ABZ37515           | AAV44436           | AAV64545           | AAZ19134           | AAZ19346           | ABL66291           | AAS94858           | AAQ84658           | AAV42686           | AAA71704           | AAD39956           | ABZ58367           |
|           |             | BB :   | т                  | ۲        | 7                  | 7                  | -                  | 7                  | 7                  | 7                  | 7        | 7                  | 7        | 7                  | ď                  | ~                  | ~                  | 7                  | 9                  | 9                  | N                  | N                  | т                  | 9                  | 7                  |
|           |             | Length | 1276               | 1258     | 6873               | 4090               | 2075               | 114955             | 2000               | 1032               | 114955   | 987                | 59816    | 59816              | 400                | 400                | 400                | 400                | 14800              | 14835              | 7175               | 7175               | 7175               | 7175               | 7117               |
| dip       | Query       | Match  | 99.1               | 96.6     | 62.6               |                    | 10.5               | 4.6                | •                  | 4.2                | 4.1      | 4.0                | 4.0      | 4.0                | -:                 | 3.9                | 9.8                | -                  | 9.6                | 3.9                | 3.8                | 3.8                |                    | 3.8                | 3.8                |
|           |             | Score  | 1265               | 1234.2   | 799.4              | 753.8              | 134.6              | 58.8               | 57.8               | 54.2               | 52       | 51.6               | 51.6     | 51.6               | 49.6               | 49.6               | 49.6               | Ø.                 | σ.                 | 49.6               |                    | 49                 | 49                 | 49                 | 4                  |
|           | Result      | No.    | 1                  | 7        | e                  | 4                  | J.                 | v                  | 7                  | σο                 | 0        | 10                 | c 11     | 12                 | 13                 |                    | 15                 | 16                 | 17                 | 18                 | 19                 |                    | 21                 |                    | 23                 |

| o i      | Aad3/81/ Sequence       |          | Aaa71703 Human cal | Aad39955 Human cal | Abl65869 Lung canc | Abz58366 Human N-t | Aax88001 N-type ca | Aas08693 Micromono | Aak92108 Human cDN | Aak93547 Human cDN | Aak94827 Human ful | Continuation (40 o | Abl32253 Human imm | Ab192203 Chemicall | Adb68842 Minority | Ada71056 Rice qene | Aaq62837 GGF gene | GGF      | Huma     | Aat48077 Human gli |
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| AAV29059 | AAQ3 / 81 /<br>AAQ84657 | AAV42685 | AAA71703           | AAD39955           | ABL65869           | ABZ58366           | AAX88001           | AAS08693           | AAK92108           | AAK93547           | AAK94827           | AAI99683 39        | ABL32253_          | ABL92203           | ADB68842          | ADA71056           | AAQ62837          | AAQ58330 | AAT30988 | AAT48077           |
|          | 7362 2                  | 62 2     | ~                  | ~1                 | 7364 6             |                    | 7376 2             |                    | 524 4              | 524 4              | 1769 4             | 00 4               | 5944 6             | 944 6              | 536 9             | m                  | 745 2             | 745 2    | īŪ       | 745 2              |
| 72       | 7.3                     | 736      | 736                | 736                | 73                 | 73                 | 73                 | 109519             | S                  | S                  | 17                 | 110000             | 59                 | 59                 | S                 | 138                | 7                 | 7        | 7        | 7                  |
| ю.<br>6  | , w                     | 3.8      | 3.8                | 3.8                | 3.8                | 3.8                | 3.8                | 3.8                | ٠.                 | 3.8                | 3.8                | 3.8                | 3.7                | 3.7                | 3.7               | 3.7                | 3.6               | 3.6      | 3.6      | 3.6                |
| 9,4      | 4. 4<br>V Q             | 49       | 449                | 49                 | 49                 | 49                 | 49                 | 49                 | 48.2               | 48.2               | 48.2               | 48                 | 47.6               | 47.6               | 46.8              | 46.8               | 46.6              | 46.6     | 46.6     | 46.6               |
| 24       | 7 7                     | 27       | 28                 | 53                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                 | 42                | 43       | 44       | 45                 |
|          |                         |          |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | υ                 |                    | υ                 | υ        | υ        | O                  |

## ALIGNMENTS

AAD00294 standard; cDNA; 1276 BP AAD00294; 

(first entry) 05-SEP-2000

Mouse oocyte-specific 01-180 cDNA clone.

Oocyte-specific; ovary; O1-180; mouse; gynaecological; treatment; screen; cell proliferative disorder; cell degenerative disorder; contraceptive; modulator; signalling pathway; human infertility; cancer; ovulation; ss.

Mus sp.

Location/Qualifiers 28. .1113 /\*tag= a Key

/product= "Mouse oocyte-specific protein, 01-180"

WO200024755-A1

04-MAY-2000

99WO-US025209. 28-OCT-1999; 98US-0106020P. 28-OCT-1998; (BAYU ) BAYLOR COLLEGE MEDICINE.

Matzuk MM, Wang P;

WPI; 2000-350684/30. P-PSDB; AAY70948. 01-180, 01-184 and 01-236 polypeptides and nucleic acids encoding them, useful for evaluating potential contraceptives to block ovulation in a reversible manner.

Claim 2; Fig 1; 54pp; English.

The present sequence is the CDNA encoding the mouse occyte-specific protein Ol180, expressed in the occytes of primary (one-layer) preantral follicles through ovulation. It provides in vitro and in vivo reagents for studying ovarian development and function. This sequence has

1080 1079 1139

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New ovary-specific-genes comprising O1-180 or O1-236, useful for decreasing conception or enhancing fertility, or for the preparation of composition for treating e.g. cancer.
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(pos:1004. .1007, aa:Phe)
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gynaecological and contraceptive activity. Agents which modulate 01-180, 01-184 and 01-236 may be used to treat cell proliferative or degenerative disorders, associated with abnormal expression of these ovary specific genes. This ovary-specific sequence can be used as reagents to evaluate potential contraceptives, to block ovulation in a reversible manner. It is also used to screen for genetic mutations in signalling pathways, that are associated with some forms of human infertility or gynaecological
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                                       The present sequence is that of murine ovary-specific 01-180 cDNA obtained from a mouse ovary CDNA library. 01-180 clones were initially identified in a subtractive hybridisation screen using ovaries from Gdf9 knockout and wild-type mice. The 01-180 gene (see AB224590) on chromosome can be operated. The invention provides ovary-specific and ocyte-specific murine and human 01-180, 01-184 and 01-236 polynucleotides and copyedides. These genes and their protein products appear to relate to various cell proliferative or degenerative disorders, sepecially those involving ovarian tumours, such as germ line tumours and gramulosa cell rolliferation of a cell proliferative or degenerative or degenerative or degenerative of seconds. The invention crowdides a method for detection of a cell proliferative or degenerative disorder of the ovary, which is associated with the expression of 01-180, 01-184 or 01-236. It also provides a method for treating such disorders by using an agent which supersess or enhances the respective activities continues that the expression of of 1180, 01-184 or 01-256, and a method of screening for compounds that the expression of interact and/or modulate the expression or activity of the ovary-specific chance these compounds are presented and provides a method for the ovary specific chances.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1258 BP; 261 A; 392 C; 392 G; 213 T; 0 U; 0 Other;
Disclosure; Page 106-107; 141pp; English
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62.6%; Score 799.4; DB 7;
Best Local Similarity 99.9%; Pred. No. 8.1e-180;
Matches 800; Conservative 0; Mismatches 1;
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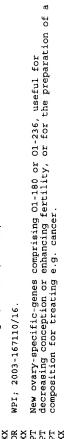
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                                                                                                                                                                                                                                                                                                                                                 New ovary-specific-genes comprising O1-180 or O1-216, useful for decreasing conception or enhancing fertility, or for the preparation of composition for treating e.g. cancer.
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Best Local Similarity
Matches 781; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1206
                                                                                                                               polynucleotides and polypeptides. These genes and their protein products appear to relate to various cell proliferative or degenerative disorders, especially those involving ovarian tumours, such as germ line tumours and gramulosa cell tumours, or infertility, such as premature ovarian tailure. The invention provides a method for detection of a cell proliferative or degenerative disorder of the ovary, which is associated with the expression of 01-180, 01-184 or 01-236. It also provides a method for treating such disorders by using an agent which suppresses or enhances the respective activities of 01-180, 01-184 or 01-236, and a method of screening for compounds that interact and/or modulate the expression or activity of the ovary-specific genes. These compounds are possible contraceptive or fertility enhancing agents. The modulator is preferably a polypeptide, small molecule or polymucleotide sequence
                                                               polymucleotide. In mice, loss of O-180 is associated with female infertility and subfertility. The invention provides ovary-specific and occyte-specific murine and human O1-180, O1-184 and O1-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmorary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmorary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGC
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                                                 present sequence is that of a human ovary-specific 01-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2075 BP; 588 A; 413 C; 473 G; 601 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 134.6; DB 7;
Pred. No. 6.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
    Claim 2; Page 136-137; 141pp; English.
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Best Local Similarity 71.1%;
Matches 207; Conservative
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and

codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

conditions or mixtures. The antisense oligonucleotides may be derived

from sequences AAX5512-74. These multiple target oligonucleotides

conditions or mixtures. Typical diseases and conditions are those

classess and conditions. Typical diseases and conditions are those

caspociated with impaired respiration and inflammation, including lung

diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,

catute asthma, allergies, asthma, impeded respiration, respiratory

distress syndrome, pain, cystic fibrosis, pulmonary hypertension,

culon cancer, breast cancers such as leukemias, lymphomas, carcinomas e.g.

colon cancer, breast cancers uning cancer, melanoma, hepatic metastases, as

colon cancer, breast which may metastasize or have metastasized

colon cancers with mixture and ancer, and ancer, melanoma, hepatic cancers as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104997 GSNNNDNNBGGCCBGGGGGCGCCGGCCGGCCGSNNNDNNGGCCBGGGCGCCCCC 105056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCCCCC--GACGCCTCGGTGCTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGGGCGCCGCACGCTGCAGGCTGCAGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 58.8; DB 2;
32.6%; Pred. No. 0.0025;
Live 71; Mismatches 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 37; 120pp; English
                                                                          97US-0059160P.
98WO-US019419
                                                                                                                                                                                                          (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.69
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasoconstriction
    17-SEP-1998;
                                                                                                                           19-JUN-1998;
                                                                                   17-SEP-1997;
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                                                                                                                                                                                                                                                                                                  Nyce JW;
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104756

182

104816

421 GCCCCGTTCTCGTCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGC 480

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105057 GGCCGGGCCGSNINIDINIGCCBGGGCGCGCCGGCCGGCCGSNINIDINICCBGGGCGCG 105116
                                                                                                                                              CGCCGGCCGCCGCGCCGCCGCCGGCCGCGCGSNNNDNNCGCGCCGCCGG 105294
                                                                                                                                                                                                   CCGGCCGSNNNDNNGCGCCGCCGGCCGGCCGSNNNDNNCGCCGCCGGCCGGCCGSNN 105354
                                                          105117 CCGCCGGCCGGCCGSNNNDNNCBGGCGCGCCGC--CGGCCGGGCCGSNNNDNNBGGGC 105174
                                                                                                         AGGCAGACACCCACGAAGGGAGGGGAGCCCCGGCATCCTCGGGGACCCCGGGAACCGGAG 540
                                                                                                                                                                              GCGGCGATGCAGTCTGAGCCTGGGAGCGAGCCATGTCCTGCCGCAGAGATGGCTCAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying at least one gene involved in plant resistance or response to abthogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                  541 CCGAGAGAGGCGCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGGGGGATGTT
                                                                                                                                CAGGCTGCAGGCAGGCCGGGTGGCAGCAGCACCACCACCGGAGGACCGGAACAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                        bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                 105355 NDNNGCCGCCGGCCGGNNNDNNCCGCCGGCCGGCCGSNNNDNNCG 105405
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T, Zou
                                                                                                                                                                                                                            GACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACG
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Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goff
a Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                                                                                                                                                                                                                                                            ADA71938 standard; DNA; 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Cooper
F, Quan S, Tao
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-175290/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
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Katagiri F,
                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to

Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

illustrate the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGRMMGGKSRMSYMMWCYARGCGSCKRKKSKGGSWGKTCRRGARGGSGWSSGAKYKSGSM 191
                                                                                                                                                                                                                                                TGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCC 756
                                                                                                                                                                                                                                                                                                            TCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAG 816
                                                                                                                                                                                                                                                                                                                                 TWCRSKRRSMMWKWMRKWRKWRSRSYGWYSWSYKKWMCTAYKKSYYSRWCYMYRGGGWRGAT 311
                                                                                                                                                                                                                                                                                                                                                                       TACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTGGGAGAGCGCCTATGTGTGGTGT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGCAGGGCACCAGTAAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTA 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                      937 CAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTTGTAAAAGAACTAGATGTGCCTG 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : :::::::: | | : | | 430 GCMTCRMKSYGMMRWKSWKRWASKYKHMSRMYRWRKKKCSRTTMMGKTRGGMMGT---MG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 WMYYMSKYTYAKYGSYMRYRYRAMCMYMMRWYYYRRSYMTYMAWYTSSTRMAMTGMKYS 726
                                                                                             71
                                                                                | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | CSSWRGRREMYMAGMMSCARMGSSRMSRKMGSMSKYRKCSSCGKCWTTRRKSKWYSASS
                                                             CTCGGGGACCCGGGAACCGGAGCCGAGAGGTGGCCGCG-AGGAAAGCGGTCCCCCAGC
                                                                                                                        578 CGCGAAGCGAGGAGGCGATGTTCAGGCTGCAGGCCGGGCCGGGTGGGAGCAGCCAC
                                                                                                                                                     72 ASGRIGSKWSSGSYSGKGMKKRYKRSKRWRGRGRRGMRRSRMRWMGRYRRCARSGRMAGG
                                                                                                                                                                                     CACCGGAGGACCGGAACAGTGTGGCGGCGAT-GCAGTCTGAGCCTGGGAGCGAGGAGCCA
                                                                                                                                                                                                                                                                  SKRMMMSSCGRSGCGRRSAYSRYYGTSKXGTYKKMTYYSASRCMRAYMTTSYSWACSSY
                                                                                                                                                                                                                                                                                                                                                                                         547 KGYYWAGMWMKRYKRMYKRMWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMCKRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .057 ATGCAAGGACAAACGCCTGTCCTGCGACAGCTTCAGCTTCAAATACATCATTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 MSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGSMKSTCT
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterial infection; fungal infection; viral infection; rice; ds.
                                 7;
    Length 2000;
 ch 4.5%; Score 57.8; DB 7; Length 2
| Similarity 10.4%; Pred. No. 0.0012;
79; Conservative 358; Mismatches 315; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRYWISWYKYCKCSWKYRSWWYYWSWWWAKIWKMWRRYA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 1032
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Query Match
Best Local S
Matches 79
                                                             519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 TGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGGATCGGGTTCCTGTCAACCCCGTG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCACGCCGGCGGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTCTCGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGCGATGTTCAGGCTGCAGGGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 CCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 AGAAGAAGCGGCCTCACGCCGGAGCAGTGCATCTGCTGGAGAGGGGCTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                             Hou Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54.2; DB 7; Length 1032; Pred. No. 0.007; 0; Mismatches 328; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1032 BP; 189 A; 331 C; 394 G; 118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                             SA, Hou
Zhu T,
                                                                                                                                                                                                                                             Goff
S Z,
                                                                                                                                                                                                                                             Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 2910; 899pp; English.
                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                             Cooper B, S, Tao Y,
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                                                                                             2001WO-IB001105.
                                                                                                                                                2001WO-IB001105.
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                                                                                                                                                                                                                                                Chen W, Co
                                                                                                                                                                                                                                                                                                                      WPI; 2003-175290/17.
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Best Local Similarity
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WO2003000898-A1
                                                                                                  22-JUN-2001;
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                                                                                                                                                                                                                                                Chang H, Ch
Katagiri F,
                                                 03-JAN-2003
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The specification describes antisense oligomucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, mixtures. The antisense oligonucleotides may be derived
from sequences AAX55272-74. These multiple target oligonucleotides
conditions or mixtures. The nultiple target oligonucleotides
from sequences AAX55180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
disease (COPD), and cancers such as leukemias lymphomas, carcinomas e.g.
colon cancer, bareast cancer, lung cancer, pancreatic cancer,
chepatocellular carcinoma, kidney cancer, metastasize or have metastasized
colon cancer, breast cancer, und cancer, metastasized
colon cancer, breast cancer, lung cancer, metastasized
colon cancer, pancers which may metastasize or have metastasized
colon cancer, pancers which may metastasize or have metastasized
647 CGGCGTTCGAGGAGCAGCAGCAGCAGGTGAAGGCCGAGGACAGGCTGAGCACAGGCA 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; und cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                 target; antisense treatment;
                                                                                                                                                                                                                                                                                                         Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                     pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                      lung disease;
                                          677 AGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGG
                                                                                GCGGCGCGCGCGCTGGACACGGACGCGCAACTGG
                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; multiple impaired respiration; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                      BP
                                                                                                                                                                                      AAX53491 standard; DNA; 114955
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     DB 2; Length 114955;
                           Pred. No. 0.1;
50; Mismatches 456; Indels
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4.1%; Score 52; 32.3%; Pred. No.
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                        Best Local Similarity Actor Matches 244; Conservative
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The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of a nucleic acid encoding avilamycins synthesis enzymes from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-ABZ37516)

and

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Bechthold

Trefzer A,

Muchlenweg A,

Weitnauer G,

WPI; 2003-018650/01. P-PSDB; ABP76728.

AG

(COMB-) COMBINATURE BIOPHARM

2001DE-01009166.

25-FEB-2001;

24-AUG-2001; 2001WO-EP009815.

06-SEP-2002

New avilamycin derivatives, useful for treatment of infections, nucleic acid encoding avilamycin synthesis enzymes.

Claim 13; Page 244-248; 319pp; German

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 TCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGGCAC
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                                        4.0%; Score 51.6; DB 7; Length 987; ral Similarity 49.6%; Pred. No. 0.029; Conservative 0: Mismatthe
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Sequence 987 BP; 121 A; 358 C; 371 G; 137 T; 0 U; 0 Other;
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1; antibacterial; virucide; protozoacide; fungicide; infe Staphylococcus aureus; biosynthetic gene cluster; gene;

Streptomyces viridochromogenes

Avilamycin;

medicine;

WO200268436-A1

Streptomyces viridochromogenes AviG4 encoding polynucleotide

(first entry)

26-FEB-2003

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tuberculosis; strain Erdman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US018214
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                                                                                            2003-018650/01
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                               Weitnauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998
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09-NOV-1998
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                                                                                                                                                                                                                            The invention relates to avilamycin derivatives (1) with antibacterial, virucide, protozoacide and fundicide activity. (1) are useful for treatment of infections (Dacterial, viral, proctozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aurens. (1) are more hydrophilic than known avilamycins. The present sequence is that of a nucleic acid encoding avilamycins synthesis enzymes from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosynthetic gene cluster; gene; ds.
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                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                      Sequence 59816 BP; 8760 A; 21053 C; 21088 G; 8915 T; 0 U; 0 Other;
                                                                                                                                                             useful for treatment of infections,
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                              Score 51.6; DB 7; Length 59816; Pred, No. 0.11; 0; Mismatches 134; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces viridochromogenes Avi gene cluster sense strand
                                                                                             Bechthold A;
                                                                                                                                                                            nucleic acid encoding avilamycin synthesis enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCTGCAGGGTGCCGAGCCAGCCCC 345
                                                                                              Trefzer A,
                                                                                                                                                                                                      Example 1; Page 68-301; 319pp; German
                                                                                                                                     P-PSDB; ABP76680, ABP76681, ABP76682
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                                       25-FEB-2001; 2001DE-01009166
                                                                   COMBINATURE BIOPHARM
                                                                                                                                                                                                                                                                                                                                                                                4.08;
              24-AUG-2001; 2001WO-EP009815
                                                                                            Muehlenweg A,
                                                                                                                                                              New avilamycin derivatives,
                                                                                                                                                                                                                                                                                                                             cluster (ABZ37515-ABZ37516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.6
Matches 132; Conservative
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                                                                                                                        2003-018650/01
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                                                                                              Weitnauer G,
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of a nucleic acid encoding avilamycin synthesis enzymes from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene
                                                                                                                                                                                                                                                                                                                                                                                   invention relates to avilamycin derivatives (I) with antibacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59816 BP; 8915 A; 21088 C; 21053 G; 8760 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                 infections,
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                                                                                                             Bechthold A;
                                                                                                                                                                                                                                              treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis; infection; diagnosis; antigen; XP22;
                                                                                                                                                                                                                                                                        nucleic acid encoding avilamycin synthesis enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51.6; DB 7;
Pred. No. 0.11;
); Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen XP22 5' DNA
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                                                                                                             Trefzer A,
                                                                                                                                                                                                                                              useful for
                                                                                                                                                                                                                                                                                                                                  Example 1; Page 68-301; 319pp; German
                                                                                                                                                                                           P-PSDB; ABB98398, ABP76678, ABP76679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                      (COMB-) COMBINATURE BIOPHARM AG.
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25-FEB-2001; 2001DE-01009166
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                                                                                                          Muehlenweg A,
                                                                                                                                                                                                                                                    avilamycin derivatives,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cluster (ABZ37515-ABZ37516)
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(first entry)
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45659

139

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45719

199

45779

259

319

Houghton R;

Campos-Neto A,

Dillon DC, C DR, Lodes MJ;

Skeiky YAW, , Twardzik

Vedvick TS,

Reed

t

(CORI-) CORIXA CORP.

WPI; 1998-261042/23.

96US-00730510. 97US-00818112. 97WO-US018293

07-OCT-1997; 11-OCT-1996; 13-MAR-1997;

23-APR-1998

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This is the 5' region of DNA coding for an antigenic portion of Mycobacterium tuberculosis antigen XP22; 3' DNA is provided in AAV4437.

XP22 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known sequences. The invention clates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, as well as DNA sequences encoding such transfected host cells. Also claimed are methods and diagnostic kits for transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                              New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                         Houghton
                                                                                       Campos-Neto A,
                                                                                                                                                                                                                                                               Claim 4; Page 185-186; 250pp; English.
                                                                                   Dillon DC, C
  97US-00818111
                                                                              Reed SG, Skeiky YAW,
Vedvick TS, Twardzik
                                      (CORI-) CORIXA CORP
                                                                                                                                          WPI; 1998-251292/22.
  13-MAR-1997;
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CCTCGGGGACCCGGGAACCGGAGGCGAGGAGGGGGGGAAAGGGGTCCCCCAGC 577 caccidanakcaccidanakcidacidanakanacaccidaccidaccidacaccida 578 CGCGAAGCGAGGAGGCGATGTTCAGGCTGCAGGCAGGCGGGTGGGAGCAGCAGCAC 637 298 CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGCCAT 697 Gaps 0; Length 400; Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 U; 0 Other; Indels Score 49.6; DB 2; ]
Pred. No. 0.064;
0; Mismatches 134; 698 GTCCTGCCGCAGAGATGGCTCAGG 3.9%; Best Local Similarity 49.2 Matches 130; Conservative 518 458 638 ð B Pp ð à g ₽ 엄 à d

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Tuberculosis, immunogenic, soluble, antigen, protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis; ss.
                                                                                     M. tuberculosis immunogenic polypeptide XP22 5'-end DNA.
                   AAV64545 standard; DNA; 400
                                                                                                                                             Mycobacterium tuberculosis
                                                                 (first entry)
                                                               27-JAN-1999
                                           AAV64545
RESULT 14
           AAV64545
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WO9816646-A2

diagnosis; detection; infection; antibody; immunisation;

Mycobacterium tuberculosis.

WO9942118-A2 26-AUG-1999

immunity; ss.

vaccine;

M. tuberculosis recombinant antigen DNA encoding 5' XP22.

(first entry)

AAZ19134;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 caccaccidacon de constante 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes an immunogenic portion of a soluble Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 CCTCACTGGAGGTTGCGGGAGGCAGGCACACCCACGAAGGGAGAGGGAGCCCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 CCTCGGGGACCCGGGAACCGGAGAGAGGTGGCCGCGAGAAAGGGGTCCCCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.6; DB 2; Length 4
Pred. No. 0.064;
0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              698 GTCCTGCCGCAGAGATGGCTCAGG 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638
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                                                                                                                                                                                                                                                               This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 CGCGAAGCGAGGAGGAGGATGTTCAGGCTGCAGGCAGGCCGGGTGGGAGCAGCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                     Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.9%; Score 49.6; DB 2; Length 400; Best Local Similarity 49.2%; Pred. No. 0.064; Matches 130; Conservative 0; Mismatches 134; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     Claim 4; Page 215-216; 323pp; English.
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          99WO-US003265
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                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                        WPI; 1999-527416/44
           17-FEB-1999;
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Search completed: September 24, 2004, 17:34:43 Job time : 587 secs us-09-830-810a-1.rni

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Sequence 12, Appl
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Sequence 179, App
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2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
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GenCore version 5.1.6
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US-08-956-8

US-08-956-18

US-08-956-18

US-08-13-118-1

US-09-268-163-7

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US-08-713-118-1
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                                                                                                                                                                                                                                                                                                                                      682709 seqs, 277475446 residues
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                                                                           nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Sequence 7, Appli
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LOCATION: .3392, 3396..3488, 3455..3539, 3543..3581, 3585
LOCATION: .3587, 3591..3562, 3630..3669, 3693..3737, 3744
LOCATION: .3746, 3750..4823, 4827..4841, 4845..5006, 5010
LOCATION: .5096, 5100..5306, 5310..5366, 5370..5465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harder, Michael
APPLICANT: Blis, Steven
APPLICANT: Blis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder. Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 12:
                                                                                   US-09-103-840A-2

US-09-103-840A-2

US-08-469-559B-163

US-08-469-5569-163

US-08-749-322A-163

US-08-74-591A-163

US-08-74-1018-51

US-08-74-163

US-08-73-163

US-08-73-163

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US-08-74-163

US-08-74-163

US-08-47-602-163

US-08-47-602-163

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US-08-47-602-163

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US-09-268-163-3
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135 S. LaSalle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/07745206A Patent No. 5429921 GENERAL INFORMATION:
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LENGTH: 5467 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
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CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 CTGTCAACCCCGGTGGCCACGGGGGCGGGAGATCCCCGGGATCCTGGCAGACCGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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.3392, 3396..3488, 3495..3539, 3543..3581, 3585
.3587, 3591..3626, 3630..3689, 3693..3737, 3744
.3746, 3750..4823, 4827..4841, 4845..5006, 5110
.5096, 5100..5306, 5310..5366, 5370..5465)
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| Patent No. 5670367 |
| GENERAL INFORMATION: | APPLICANT: PORNER, F. |
| APPLICANT: SCHENFLINGER, F. |
| APPLICANT: FALKNER, F. G. |
| TITLE OF INVENITION: RECOMBINANT FOWLPOX VIRUS |
| NUMBER OF SEQUENCES: 52 |
| CORRESPONDENCE ADDRESS: | ADDRESSE: Foley & Lardner |
| STREET: 1800 Diagonal Road, Suite 500 |
| STREET: 1800 Diagonal Road, Suite 500 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 2; Pred. No. 0.00037;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
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                                                                                                                                                                                                                                                                                               DNA (genomic)
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Best Local Similarity 46.7%;
Matches 171; Conservative (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                             5467 base pairs
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 unknown
                                                                                                                    Leic acid
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STATE:
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TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
            Score 54; DB 1; Length 5467;
Pred. No. 0.00037;
0; Mismatches 195; Indels
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APPLICATION NUMBER: US/08/311,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown, Martin, Haller & McClain
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APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
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Patent No. 5876598
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
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TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
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INFORMATION FOR SEQ ID NO: 12:
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Ellis, Steven
Williams, Mark
Feldman, Daniel
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COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   Matches 171; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma:
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STREET: 160 CITY: San Diego
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                                          Query Match
Best Local Similarity
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Best Local Similarity 6.5%; Pred. No. 0.00068;
Matches 25; Conservative 202; Mismatches 155; Indels
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Patent No. 6229000
GENERAL INFORMATION:
APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                               30472/114 IMMU
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                                                                    APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
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TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: single
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US-08-232-463-14
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IMMEDIATE SOURCE:
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STREET: 650
CITY: Tarrytown
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1636 GAGGCCCGAAAGGCGGAGAGAGCGGGAGCCCGGTGCCCGGAAGAAGAGGGGCCGCGCCGCAC 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 GIGGCCGCGGAGAAAGCGGICCCCCCAGCCGCAAGCGAAGGGGCGAIGITCAAGGTGCA 609
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COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayer 8398.3-KGB
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/456,200B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/094,712
FILING DATE: 19-JUL-1993
PRIOR APPLICATION NUMBER: 07/858,278
FILING DATE: 26-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/858,778
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,778
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 41 10 785
FILING DATE: 04-APR-1991
                                                                                                                                     COMPUTER: NEC Powermate SX/20 OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Baye
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                         SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
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(914) 332-1844
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Pred. No. 0.0015;
                                            APPLICANT: Gampos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Oodes, Michael J.
APPLICANT: ANTERNON: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
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; Sequence 179, Application US/09072967
; Patent No. 6592877
; GENERL INFORMATION:
; APPLICANT: Sked, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
Skeiky, Yasir A.W.
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Best Local Similarity 49.2'
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 400 base pairs
nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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TOPOLOGY:
US-09-072-596-174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 CCTCACTGGAGGTTGCGGGAGGCAGGCACCCCACGAAGGGAAGGGAGGCCCGGCAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGAAGCGAAGGAGGCGATGTTCAGGCTGCAGGCCGGGCCGGGTGGGAGCAGCAGCCAC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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49.2%; Pred. No. 0.0015;
tive 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 GTCCTGCCGCAGAGATGCCTCAGG 721
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                                                                                                                                                           Sequence 179, Application US/09056556; Patent No. 6350456; Patent Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS AND ME NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 174, Application US/09072596; Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPEX: (206) 682-6631
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 130; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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STATE: Washingtor
COUNTRY: USA
ZIP: 98104-7092
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                                                                                         RESULT 5
US-09-056-556-179
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APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
ITILE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown ::
STRDEN
                                                                                                                                                                                                                                                                                                                                    E: Brown, Martin, Haller & McClain
1660 Union Street
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OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING DATE:
PLING DATE:
PRING DATE:
OPERATE:
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OPERATE:
OPERATION NUMBER:
OPERATE:
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COMPUTER READABLE FORM:
MEDIUM TYPES. Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                            San Diego
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
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US-08-455-543A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 CCTCACTGGAGGTTGCGGGAGGCAGGCAGACACCCACGAAGGGAAGGGAGAGCCCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 CCTCGGGGACCCGGAACCGGAGCCGAGGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGC
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                                                                                                        APPLICANT: Campos. Netco, Antonio
APPLICANT: Campos. Netco, Raymond
APPLICANT: Vedvick. Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%; Score 49.6; DB 4; Length 400;
49.2%; Pred. No. 0.0015;
tive 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIPICATION:
NAME: MAKL, DAVId J
REGISTRATION NUMBER: 31,392
REFERRANCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                698 GTCCTGCCGCAGAGATGGCTCAGG 721
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Sequence 8, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
                                                                                      Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                355
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 49.2'
Matches 130; Conservative
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ADDRESSEE: SEED and E
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
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Score 49; DB 1; Length 7175; Pred. No. 0.0085;

3.8%;

Query Match Best Local Similarity

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MOLECULE TYPE: DNA (genomic)
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                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTER.STICS: LENGTH: 7.175 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8
Query Match
Best Local Similarity 48.0
Matches 201; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma
619-238-0062
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                                                                                                                                                                                                                                                                                                                                                                       CDS
144..6857
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STATE: California
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ZIP: 921
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LOCATION:
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FEATURE:
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US-08-193-078B-8
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                                                                                     250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGTCGGTGCAGTGTTCACTCGGGCGC
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APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
            0; Mismatches 215; Indels
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STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: T
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
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IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
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Williams, Mark
Feldman, Daniel
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TITLE OF INVENTION: METHOI
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
                     201; Conservative
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MEDIUM TYPE: Floppy
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SOFTWARE: PatentII
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Sequence 8, Application US/08223305C
Batent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Elliams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
ANAMADED OF GENTUMANCE: FT
Score 49; DB 2; Length 7175; Pred. No. 0.0085;
                                                                   Mismatches 215;
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1660 Union Street
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1048 GCGGAGAGCGGGAGCCGCGCGCGCGCCCGGCCCCGGCACAAGGCGCAGCCTGCT 3107
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                                        490 CCCACGAAGGGAGGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGGCGGAGAAG
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APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 40
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,097D
FILING DATE: 05-NOV-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION NUMBER: WO PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US DEPLICATION NUMBER: US DEFLICATION NUMBE
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FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
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FILING DATE: 13-UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
OFFICE AND MINER. US 07/176,899
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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: California
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APPLICANT: Harpol
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92101-2926
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Pred. No. 0.0085;
0; Mismatches 215; Indels
                  MOLECULE TYPE: DNA (genomic)
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3.8%;
Best Local Similarity 48.0%;
Matches 201; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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; LOCATION:
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APPLICANT: Gillespie, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0085;
0; Mismatches 215; Indels
                                                                                                       ALICAMENTAL STATES OF THE STAT
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Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
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Ellis, Steven
Williams, Mark
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Best Local Similarity 48.0%;
Matches 201; Conservative
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
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LOCATION:
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; LOCATION:
US-08-149-097D-8
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Pred. No. 0.0085;
0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
FILING DATE:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/290,012

FILING DATE: 11-AUG-1994

APPLICATION NUMBER: 08/149,097

FILING BATE: 5-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/105,536
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FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (619) 238-0999
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 bace
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Best Local Similarity 48.0%;
Matches 201; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6855.,7175
                                                                                                                                                                                                                                                       ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144..6857
                                       STREET: lobv.
CITY: San Diego
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1..143
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LOCATION:
FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-450-562-8
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3048 GCGGAGAGCGCGGCGGCGGCGCGCCCGGCCCGGCACAAGGCGCACCTGCT 3107
                                                                                             610 GGGCAGGCCGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGGAT 668
                                                                                                                                                                                                                                             APPLICANT: Blis, Steven
APPLICANT: Elis, Steven
APPLICANT: Milliams, Mark
APPLICANT: McOue, Ann
APPLICANT: Gillespie, Alison
APPLICANT: Gillespie, Alison
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCI/US92/06903
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PRIOR APPLICATION DATA;
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
FILING DATE: 7-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEP7-1994
FILING DATE: 28-SEP7-1994
PRIOR APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEP7-1994
PRIOR APPLICATION NUMBER: 08/290,012
APPLICATION NUMBER: 08/290,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-ARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
                                                                                                                                                    RESULT 13
US-08-450-562-8
; Sequence 8, Application US/08450562
; Patent No. 6096514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: 08/105,536
11-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/868,354
FILING DATE: 10.APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-JULY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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2751 dAGGCCCCGAAAGGCGGAGAGCGGGGAGCCCGGTGCCCGGAAGGAGCGGCCGCGGCCGCAC 2810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2928 GAĠCGGĠAĠCĊĊCGACĠCCAĊĊGĊGCAĊCGGĊACCAĠĠAŢCĊĠAĠCAAGGAĠTGCGĊC 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3048 dcddagaccdddadadcccdcddcddcaccdddaccccdcadadgcccidcr 3107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 GACGCTGCGGTGCAGGTGAACCCGCGCCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 CCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCGTTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 CCCACGAAGGGAGGGGGGGCCCCGGCATCCTCGGGGACCCGGGAACCGGAAGCGAAGAGAG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550 GIGGCCGCGAGGAAAGCGGICCCCCAGCCGCGAAGCGAGGAGGCGAIGITTCAGGCTGCA 609
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3.8%; Score 49; DB 3; Length 7175;
Best Local Similarity 48.0%; Pred. No. 0.0085;
Matches 201; Conservative 0; Mismatches 215; Indels
FILING DATE: 14-AUGL-1,2,2

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 08-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 08-NOY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 33,779
FILING DATE: 04-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
FRIENCE/POCKET NUMBER: 6562-519812
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEPRAN: (619) 238-0999
TELEPRAN: (619) 238-0999
TELEBRANCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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550 GIGGCCGCCAAGAAAGCGGTCCCCCAGCCGAAGCGAGGAGGAGGATGITCAGGCTGCA 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 GGGCAGGCCGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCCGCAT 668
                                                                                                                                                                             490 CCCACGAAGGGAGAGGGGGGGCTCCTCGGGGACCCGGGAACCGGAGCCGAAGAGA
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US-08-450-272-8

US-08-450-272-8

US-08-450-272-8

US-08-450-272-8

US-08-450-272-8

Sequence 8, Application US/08450272

Patent No. 6387696

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Williams, Mark

APPLICANT: Williams, Mark

APPLICANT: Gillespie, Alison

APPLICANT: Redman, Daniel

APPLICANT: Redman, Daniel

APPLICANT: METHODS

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Mark

STREFT:

ATREFT:

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OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,272
FILING DATE:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/314,083
FILING DATE: 20-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 20-SEPT-1994
PRIOR APPLICATION NUMBER: 08/311,363
FILING DATE: 20-SEPT-1994
PRIOR APPLICATION NUMBER: 08/311,363
FILING DATE: 21-SEPT-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
CLASSIFICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
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APPLICATION DATA:
APPLICATION NUMBER: 08/23,305
FILING DATE: 4-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: California
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APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & MCAuliffe STRES: ADDRESSEE: Heller Ehrman White & MCAuliffe CITY: La Johla
STREE: California
COUNTY: La Johla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDISkette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRAATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE (619) 587-5360
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 715 base pairs
TYPE: nucleic acid
STEANBEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.8%; Score 49; DB 4; Length 7175;
Best Local Similarity 48.0%; Pred. No. 0.0085;
Matches 201; Conservative 0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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6855..7175
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1..143
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LOCATION:
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FILING DATE: 5-NOV-1993

PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993

PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/914,231
FILING DATE: 13-ULY-1992
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06903
FILING DATE: 14-AUG-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 6362-519812
FILING DATE: 15-AUG-1991
CLASSIFICATION: 33,779
FILING DATE: 15-AUG-1991
CLASSIFICATION: 135
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie I.
REGISTRATION NUMBER: 619) 238-0999
TELLEPHORE: (619) 238-0999
TELLEPAN: (619) 238-0962
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERESTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDENDESS: double
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MOLECULE TYPE: DNA (genomic)
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144..6857
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